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P42359 streptococc
P52340 human herpe
P52345 saccharomyc
P30002 human herpe
Q03640 saccharomyc
O51063 borrelia bu
Q03470 campylobact
Q60290 methanococc
P50620 bacillus su
P81021 gallus gall
P55155 caenorhabdi
Q05808 anthonomus
P50640 mycobacteri
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P97739 cavia
Q61391 mus mu
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P08473 homo sapien
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007744 lactococcus
009145 lactococcus
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VARIANTS HYP ARG-160 AND ASN-444 INS
                                   patients with hypophosphatemic rickets.
Hum. Mutat. 15:383-384(2000).
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MEDLINE-99368844; PubMed-10439971;
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Holm I.A., Huang X., Kunkel L.M.;
"Mutational analysis of the PEX gene in patients with X-linked
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"A gene (PEX) with homologies to endopeptidases is mutated in patients with X-linked hypophosphatemic rickets. The HYP
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SEQUENCE OF 4-641 FROM N.A.
MEDLINE-96024647; PubMed-7550339;
                                                                                                                                                                                                                                    J., Pannetier S., Garnier J.-M., Rowe P.S.N., Francis ne A., Hanauer A., Econs M.J., Oudet C.L.;
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Genet. 6:539-549(1997).
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Matches
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prof.669; p97439;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating neutral endopeptidase) (X-linked hypophosphatemia protein) (HYP)
(Vitamin D-resistant hypophosphatemic rickets protein).
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           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                 PHEX OR PEX OR HYP
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Du L., Desbarats M., Viel J., Glorieux F.H., Cawthorn C., Ecarot "cDNA cloning of the murine Pex gene implicated in X-linked hypophosphatemia and evidence for expression in bone."; Genomics 36:22-28(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96411643; PubMed=8812412;
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SEQUENCE FROM N.A.
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EMBL; U73910;
EMBL; U73912;
EMBL; U73913;
EMBL; U73914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pex/PEX tissue distribution and evidence for a deletion in the 3 region of the Pex gene in x-linked hypophosphatemic mice.";
J. Clin. Invest. 99:1200-1209(1997).
J. Clin. ENOBABLY INVOLVED IN BONE AND DENTIN MINERALIZATION AND REMAL PHOSPHATE REABSORPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=97217775; PubMed=9063736;
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ACT_SITE
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Interpro; IPR001230; Prenyl_site.
Interpro; IPR001330; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
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U75646; AAB47750.1;
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N-LINKED
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ZINC (CATALYTIC) (BY SIMILARITY)
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
(Enkephalinase) (Common acute lymphocytic leukemia antigen) (CALLA)
(Neutral endopeptidase 24.11) (CD10).
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MEDILINE-89386688; PubMed-2528730;

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"Organization of the gene encoding common acute lymphoblastic leukemia antigen (neutral endopeptidase 24.11); multiple miniexons and separate 5' untranslated regions.";

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MEDLINE=20135972; pubMed=10669592;
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Le Moual H., Dion N., Roques B.P., Crine P., Boileau G.;
"Asp550 is crucial for catalytic activity of neutral endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure of human neutral endopeptidase (Neprilysin) complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shipp M.A., Richardson N.E., Sayre P.H., Brown N.R., Masteller E.L., Clayton L.K., Ritz J., Reinherz E.L.;
"Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA) identifies a type II integral membrane protein.";
Proc. Natl. Acad. Sci. U.S.A. 85:4819-4823(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maifroy B., Kuang W.-J., Seeburg P.H., Mason A.J., S
"Molecular cloning and amino acid sequence of human
(neutral endopeptidase).";
FEBS Lett. 229:206-210(1988).
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                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein.
DISEASE: IMPORTANT CELL SURFACE MARKER IN THE DIAGNOSTIC OF HUMAN
ACUTE LYMPHOCYTIC LEUKEMIA.
                                                                                                                                                                                                                                                                                            FUNCTION: THERNOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY IMPORTANT IN THE DESTRUCTION OF OPLOID PEPTIDES SUCH AS METAND LEU-ENKEPHALINS BY CLEAVAGE OF A GLIZ-PHE BOND. CAPALYTIC ACTIVITY: Preferential cleavage at the amino group of hydrophobic residues in insulfa, casein, hemoglobin, and a number
                                                                                                                                                                                                                                                                     of other proteins and polypeptides. COFACTOR: BINDS 1 ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exp. Med. 168:1247-1253(1988).
Y00811; CAA68752.1;
       X07166; CAA30157.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seeburg P.H., Mason A.J., Schofield P.
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BINDING
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InterPro; IPR001230; Prenyl_site.
InterPro; IPR0011230; Prenyl_site.
InterPro; IPR001130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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Genew; HGNC:7154; MME.
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                                                                                                                                                               13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
   73
                                                   71 NLSVDPCDNFERFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
                                                                                                         18 KKKORWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIONM 72
                                                                                                                                                                                                                                                      Local
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1DMT; 20-DEC-00.
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DATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLQE--PKTEDIV 130
                                                                                                                                                                                                                           272;
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STOP-TRANSFER SEQUENCE (P
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                                                                                                                                                                                                                                                                                    Score 1283.5; DB 1; Length 749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AVQKAKALYRSCINESAIDSRGGEPLLKLL-PDIYGWPVATEN-----WEQKYGASWTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 ALYKEMVDTAVL-----LGANSSRAEHDMKSVLRLETKIAETMIPHENRTSE-AMYNKM 300
                                                                                                                                                                                                                                                                                                                                               NEP_RABIT STANDARD; PKI; /*5 AA.

1908049;
101-AUG-1988 (Rel. 08, Created)
101-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 42.4.11) (Neutral endopeptidase) (NEP)
15-Jun-2002 (Neutral endopeptidase 24.11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 KVGYP-EFINNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 PTTVNAFYSASTNQIRFPAGELOKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
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                                                                                                                    Devault A., Lazure C., Nault C., le Moual H., Seidah N.G., Chretten M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P., Crine P., Boileau G.;
                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).

Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 GNFRIIGTLONSAEFSEAFHCRKNSYMN-PEKKCRVW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657
                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                   "Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 "Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalinase) deduced from a complementary DNA."; EMBO J. 6:1317-1322(1987).
                                                                                                                                                                        MEDLINE=87275825; PubMed=2440677;
                                                                                                                                                                                               TISSUE-Kidney
                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                (Enkephalinase) (Neutral endopeptidase 24.11).
Devault A., Lazure C., Nault C., Chretien M., Kahn P., Powell J.,
                                                                                                                                                                                                                                                                Mammalia;
                                     ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKAIAQLNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSR-DYYECTGIYKEACT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFRAYRKWINDRROGLEEPLLPGITFTNNOLFFLSYAHVRCNSYRPEAAREQVQIGAHSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYRAYQNYI--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP
                                                                                                                                                                                                                                                                Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                    Leporidae;
           le Moual H., Seidah N.G.,
Mallet J., Beaumont A., Roques B.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    749
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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InterPro; IPR001230; Prenyl_site.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=87241544; PubMed=3297057; Rahn P.H., Powell J.F., Beaumont A., Roques B.P., Mallet J.J.; "An antibody purified with a lambda GT11 fusion protein precipitates enkephalinase activity."; Biochem. Blophys. Res. Commun. 145:488-493(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Exploration of the catalytic site of endopeptidase 24.11 by site-
directed mutagenesis. Histidine residues 583 and 587 are essential for catalysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devault A., Sales V., Nault C., Beaumont A., Roques B., Crine P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88196403; PubMed=3162886;
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EMBO J. 6:2506-2506(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THEMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY IMPORTANT IN THE DESTRUCTION OF OPLOID PEPTIDES SUCH AS METAND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND. CATALYTIC ACTIVITY: Preferential cleavage at the amino group of hydrophobic residues in insulin, casein, hemoglobin, and a number
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00786; NEPRILYSIN
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metalloprotease; Zinc;
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                                                                                                              85450 MW;
                                32.1%; Score 1270.5; 36.1%; Pred. No. 6.9
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               149;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .).
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ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                         N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
STOP-TRANSFER SEQUENCE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                               E60B04357B0BABE9 CRC64;
     Mismatches
                                                                                                                                                                                                                                                                                                                                       (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
                                   .9e-78
                                                  DB 1;
          290;
       Indels
                                                  Length 749;
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19;
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NEP_RAT
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Malfroy B., Schoffeld P.R., Kuang W.-J., Seeburg P.H., Mason A.J.,
Hensel W.J.;
                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-87213218; PubMed-3555489;
                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                               P07861;
01-AUG-1988
                                                                                                                                                                                                                                                                                                    NEP_RAT
                                                                                                                                                                                                                                                                                                                                                                               714 GNFRIIGSLQNSVEFSEAFQCPKNSYMN-PEKKCRVW 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 PTTVNAFYSASTNOIRFPAGELOKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 RIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 GSERKKTIANYLVWRMYYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
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                                                                                                                                                                                                                                                                                                STANDARD;
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J. Biol. Chem. 264:6151-6157(1989).
J. Biol. Chem. 264:6151615.
J. Biol. Chem. 264:61516.
J. Biol. Chem. 264:61516.
J. Biol. Chem. 264:61516.
J. Biol. Chem. 264:61516.
J. Biol. Chem. 264:6
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Bateman R.C. Jr., Jackson D., Slaughter C.A., Unnithan S., Chai Y.G.
Moomay C., Hersh L.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and amino acid sequence of rat enkephalinase."; Biochem. Biophys. Res. Commun. 144:59-66(1987).
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METAL
ACT_SITE
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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interPro; ipR001230; Prenyl_site.
interPro; ipR000130; Zn_Mipeptdse.
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HSSP; P08473; 1DMT.
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                                                                                                                                 18 KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 72
                                                                                                                                                                                                      13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
                                                             71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
       73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
   DASAEPCTDEFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 130
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metalloprotease; Zinc; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                            51
15
102
583
584
587
646
650
144
210
210
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324
627
749
                                                                                                                                                                                                                                                                              Conservative 151; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       85663 MW;
                                                                                                                                                                                                                                                                                                               31.9%; Score 1263.5; 35.7%; Pred. No. 2e-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
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ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                         2e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ECE1_CAVPO P97739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 EKSIAQLNSKYGKKVLINFFYGTDDKNSTQHIIHFDQPRLGLPSR-DYYECTGIYKEACT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TLAKLQNNFSLEINGKPESWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKPIL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 NISELSAMI------PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AYVDEMISVARLIRQEORLPIDENQLSLEMNKVMELEKEIANATTKPEDRNDPMLLYNKM 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 ENAVGRLYVEAAFAGESKHYVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIKE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 TKYSPRDLONLMSWRFIMDLYSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNGNM 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
by guinea pig airway epithelial cells.";
Biochem. Mol. Biol. Int. 37:1001-1010(1995).

-i- FUNCTION: CONVERTS BIG ENNOTHELIN-1 TO ENNOTHELIN-1.

-i- CAPALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-

-i- CAPALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-

-i- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last annotation update) endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 AAVVNAFYSSGRNQIVFPAGILQPPFF-SARQSNSLNYGGIGMVIGHEITHGFDDNGRNF 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cranlata; vertebrata; Eutereos o
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714 GNFRIIGTLQNSAEFADAFHCRKNSYMNPER-KCRVW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 AFRAYRKWINDRROGLEEPLLPGITFTNNOLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597
                                                                                                                                                                                          Shima H., Yamanouchi M., Omori K., Sugiura M., Kawashima K.,
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                       *Endothelin-1 production and endothelin converting enzyme expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKDGDLVDWWTQQSANNFKDQSQCMVYQYGNFTWDLAGGQHLNGINTLGENIADNGGIGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYRAYQNYV--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                       PubMed=8624482;
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                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
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391 DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFGLGPMFVKATFAEDSKNIASE 450
                                                                                                         336 ---LNTIFYP--VEINESEPIVYYDKEYLEQVSTLINTTDKCLLNNYMIWNLVRKTSSFL
                                                                                                                                                                                                                                                                   263 ---NSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                   170 MNETRIEELRAKPLMELIEKLG-GWNI-----TGPWAKDNEQ--DTLQVVTAHYRTSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 FACDGWISNNPIPEDMPSYGYYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00786; NEPRILYSIN PROSITE; PS00142; ZINC_PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000718; Peptidase_M13.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 LIVLV-ALLAAGLVACLTALGIQYRTRTPPVCLSEACVSVTSSILNSMNPTVDPCQDEFS 111
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                                                   SRRFQYRWLEFSRVIQGT-TILLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
                                                                                                                                                            KKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNL
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                                                                                                                                                                                                                GDENAIRAQ--MQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF- 335
                                                                                                                                                                                                                                                                                                                         FFSVYVSADSKNSNRNVIHVDQSGLGLPSRDYYL-NKTENEKVLNGYLNYMVQLGKLLGG
                                                                                                                                                                                                                                                                                                                                                                          FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLLGA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284;
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Pred. No. 2.46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F0646C57FF2BA8A0 CRC64;
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(GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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IPR000718; Peptidase\_M13

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            MEROPS; M13.001;
MGD; MGI:97004; N
                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                  EMBL; M81591; AAA37386.1; -. HSSP; P08473; 1DMT.
                                                                                                                                                                                                                                                                                                                            endopeptidase 24.11). Molecular characterization, chromosomal localization, and modeling of the active site.";

J. Immunol. 148:2817-2825(1992).

-1- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS METAND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.

-1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of hydrophobic residues in insulin, casein, hemoglobin, and a number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEP_MOUSE STANDARD; PRT; 749 AA. Q61391; Q1-NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP) (Enkephalinase) (Neutral endopeptidase 24.11) (CD10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen C.Y., Salles G., Seldin M.F., Kister A.E., Reinher E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92242908; PubMed=1374101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 NSKEFSEHFQCPPGSPMN-PRHKCEVW 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 DRRQGLEEPILPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 PTKNEIVFPAGILPAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 ASTNOIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 VPDL----YFENAMRF-----FNFSWRVTAEQLRKAPNRDQWSMTPPMVNAYYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 IILEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 LVEGVRWAFIDMLEKENEWNDAGTKRKAKEKARAVLAKVGYPEFIM------NDTHV 488
                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                of other proteins and polypeptides. COFACTOR: BINDS 1 ZINC ION. SUBCELLULAR LOCATION: Type II membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KKNGAEE-TLPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKNSSYEAFKQQTECMYEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Common acute lymphoblastic leukemia antigen
              Mine
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CTAYYDFMISVARLIRQEQSLPIDENQLSLEMNKYMELEKEIANATTKPEDRNDPMLLYN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 SLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KKANRGT--RIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                   473 LAKVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWF 531
                                                                                                                                                                                                                                                                        417 NMENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAI 475
                                                                                                                                                                                                                                                                                                                             413 ALPYVVGKMEVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
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                                                                                                                                                              476 KERIGYPDDIISNENKLNNEYLELNYREDEYFENIIQNLKFSQSKQLKKLREKVDKDEWI 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKKQRWTPLEISLSVLV----LLXTIIAVT---MIALYATYDDGICKSSDCIKSAARLIQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVAVQKAKTLYRSCINESAIDSRGGQPLLKLL-PDIYGWPVASDN-----WDQTYGTSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMNISELSAMI-----PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDALYKFMYDTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYN 298
                                                                                                                                                                                                                                                                                                                                                                                     ILTKYSPRDLQNLMSWRFIMDLVSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMTLAKLQNNFSLEVNGKSFSWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKP 356
                                                       SGAAVVNAFYSSGRNQIVFPAGILOPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
                                                                                                         TNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGALGVIVGHEFTHGFDNNGR 591
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KYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGL 650
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
STELAC6685FDEE30 CRC64;
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9; Mismatches
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PROTON DONOR (BY SIMILARIZY).
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3.8e-77:
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RARRER REPRESENTATION OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 7-770 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   renal adenocarcinoma (ACHN) cells producing endothelin-2.";
Biochem. Biophys. Res. Commun. 208:721-727(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme (ECE-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yorimitsu K., Moroi K., Inagaki N., Saito T., Masuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE-95209687; PubMed-7695628;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valdenaire O., Rohrbacher E., Mattei M.-G.; "Organization of the gene encoding the human endothelin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A AND B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masaki T., Seino S., Kimura S.; "Cloning and sequencing of a human endothelin converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96102029; PubMed=8530372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimada K., Matsushita Y., Wakabayashi K., Takahashi M., Matsubara A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Umbilical vein endothelial cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 207:807-812(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and functional expression of human endothelin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95169128; PubMed=7864876;
MEDLINE-99421637; PubMed-10491078; MEDLINE-99421637; PubMed-1004 D., Egidy G., Thouard A., Barret A., Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A., Vranckx R., Tougard C., Michel J.-B.;
                                                                                                                                               Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                 "Human endothelin-converting enzyme-lc.";
                                                                                                                                                                                                                                                                                                                             Takayanagi R.;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM C)
                                                                                  SEQUENCE OF 1-132 FROM N.A. (ISOFORM D), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanzawa K.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUROpean Bioinformatics Institute. There are no restrictions on its modified and this statement as long as its content is in no way entitles requires a license agreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SURCELLULAR LOCATION: Type II membrane protein.
-1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A, B (SHOWN HERE), C AND D; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ALL ISOFORMS ARE EXPRESSED IN UMBLICAL VEIN CARDIOMYCCYTES AND VENTRICLES. ISOFORMS A, B AND C ARE ALSO EXPRESSED IN PLACENTA, LUNG, HEART, ADRENAL GLAND AND PHAROCHROMOCYTOMA; ISOFORMS A, AD C IN LIVER, TESTIS AND SMALL INTESTINE; ISOFORMS B, C AND D IN ENDOTHELIAL CELTS AND UMBLICAL INTESTINE; ISOFORM B, C AND D IN ENDOTHELIAL CELTS AND UMBLICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- CATALYTIC ACTIVITY: FORMS endothelin 1 by cleavage of the Trp-|-Val-22 bond in the precursor ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
-- CATALYTIC ACTIVITY. FORms CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flowers M.A., Tai S.C., Baluyut C.A., Cheung A.H., Kau C.L., Wong G.K.T., Marsden P.A.; "Characterization of the human endothelin converting enzyme-1 (ECE-1): genomic structure and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schweizer A., Valdenaire O., Nelboeck P., Deuschle U., Dumas Milne Edwards J.B., Stumpf J.G., Loeffler B.-M.; "Human endothelin-converting enzyme (ECE-1): three isoforms with distinct subcellular localizations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Blochem. 264:341-349(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEIN SMOOTH MUSCLE CELLS; ISOFORMS C AND D IN SAPHENOUS VEIN CELLS, AND ISOFORM C IN KIDNEY.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
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D49471; BAA08442.1;
X91922; CAA63015.1;
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126 FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR 183
                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                            81 FRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:3146; ECE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X98272; CAA66922.1; ---
EMBL; AL031728; CAB52285.1; ---
EMBL; AF018034; AAD21221.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M13.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600423; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; X91933; CAA63016
; X91934; CAA63016.
; X91935; CAA63016.1
; X91936; CAA63016.1
; X91937; CAA63016.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       " X91926; CAA63016.1; 

" X91927; CAA63016.1; 

" X91928; CAA63016.1; 

" X91929; CAA63016.1; 

" X91930; CAA63016.1; 

" X91931; CAA63016.1; 

" X91931; CAA63016.1; 

" X91932; CAA63016.1; 

" X91933; CAA63016.1; 

" X91934; CAA63016.1; 

" X91944; 

" X91944; 

" X919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P08473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB031742; BAA83687.1; -. AL031005; CAA19767.1; -. AL0310828; CAB46443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D43698; BAA07800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X91938; CAA63016.1;
X91939; CAA63016.1;
                                                                                                                                                                                                                                                                                             770 AA;
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000718; Peptidase_M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metalloprotease; zinc; Glycoprotein; Transmembrane;
nor; Alternative splicing; Polymorphism.

1 68 CYTOPLASMIC (POTENTIAL).
69 89 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
187
210
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1DMT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                          87163 MW;
                                                                                                                                                                                                                   31.8%; Score 1257; 37.6%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zn_MTpeptdse.
                                                                                                                                                                                                    126;
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                                                                                                                                                                                                                                                                                                                                                                                          MRGVWPPPVSALLSALG -> MEALRESVLHLALQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                              /FTId=VAR_011972
                                                                                                                                                                                                                                                                                                                                                        MRGVWPPPVSALLSALG ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRGVWPPPVSALLSALGMSTYKRATLDEEDLVDSLSEGDAY
PNG -> MPLQGLGLQRNPFLQGKRGPGLTSSPPILDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (CATALYTIC) (BY SIMILARI
ZINC (CATALYTIC) (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
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                                                                                                                                                                                                                                                                                   DD88A59748B22F80 CRC64;
                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                               I (IN DBSNP:1076669)
                                                                                                                                                                                                                   1257; DB 1;
No. 5.8e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MPLQGLGLQRNPFLQGKRGPGLTSSPPLLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. .
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(BY SIMILARITY).
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                                                                                                                                                                                                                                    Length 770;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                 M (IN ISOFORM C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                      64;
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EMBL;

EMBL; EMBL;

21;

EMBL; EMBL; EMBL; EMBL; EMBL;

X91927; X91928; X91930; X91930; X91931; X91932; X91933; X91934; X91934; X91935; X91935; X91937; X91937; X91937; X91939; X91939;

EMBL; EMBL; EMBL;

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 P42893; Q9WUY8; Q9WUY9;
01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme 1 (EC 3.4.24.71)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 LVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM------NDTHV 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
                                                                                                                                                    from
                                                                                                                                                                                      MEDLINE-94308046; PubMed-8034569;
Shimada K., Takahashi M., Tanzawa K.;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECE1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 DRROGLEEPLLPGITFTUNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 VPDL-----YFENAMRE-----FNFSWRVTADQLRKAPNRDQWSMTPDMVNAYYS 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
                                     TISSUE-Smooth muscle;
MEDLINE-99421637; PubMed-10491078;
                                                                                               SEQUENCE OF 1-116 FROM N.A.,
                                                                                                                                                                    "Cloning
                                                                                                                                                                                                                               TISSUE-Endothelial cells;
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
valdenaire O., Lepailleur-Enouf D., Egidy G.,
Vranckx R., Tougard C., Michel J.-B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 NSKEFSEHFRCPPGSPMN-PPHKCEVW 770
                                                                              LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACMNETRIEELRAKPLMELIERLG-GWNI-----TGPWAKDNFQ--DTLQVVTAHYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DORFODADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANSSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCMNEKAIEKADAKPLLHILRHSPERWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LNTIFYP--VEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKYIDTRLYPHLKDISPSENVVVRVPQYFKDLERILGSERKKTIANYLVWRMVYSRIPNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPFFSVYVSADSKNSNSVVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KKNGAEHS-LPTLGLINNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                   Chem.
                                                                                                                                                    and functional expression of endothelin-converting enzyme endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                       269:18275-18278(1994).
                                                                                                                                                                                                                                               (ISOFORM C).
                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                 ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            762 AA
                                                                                                   SPLICING,
                                                                                                                                                                                                                                                                                                                                                                                  (ECE-1).
                           Thouard A., Barret A.
                                                                                                     SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
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Eur. J. Blochem. 264:341-349(1999).
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelin-converting enzyme-1."; FEBS Lett. 371:140-144(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Lung; MEDLINE=95402196; PubMed=7672114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-109 FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from an additional promoter.
                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and characterization of two isoforms of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimada K., Takahashi M., Ikeda M., Tanzawa K.;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane protein.

ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ALL ISOFORMS ARE EXPRESSED IN AORTIC ENDOTHELIAL CELLS. ISOFORM A IS ALSO EXPRESSED IN LIVER; ISOFORM E IN SMOOTH MUSCLE CELLS, AND FIBROBLASTS; ISOFORM C IN AORTIC IN SMOOTH MUSCLE CELLS, FIBROBLASTS, LIVER AND LUNG, AND ISOFORM D IN SMOOTH MUSCLE CELLS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
TIP-1-Val-22 bond in the precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON (BY SIMILARITY). SUBUNIT: HOMODIMER (BY SIMILARITY).
D29683; BAA06152.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ш
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THE REPORT OF A CONTROL OF A CO Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane; InterPro; IPR000130; Zn\_MTpeptdse.
pfam; PF01431; Peptidase\_M13; 1. InterPro; IPR000718; InterPro; IPR000130; EMBL; METAL DOMAIN Signal-anchor; PROSITE; PS00142; ZINC\_PROTEASE; 1. MEROPS; M13.002; EMBL; CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD ACT\_SITE METAL TRANSMEM VARSPLIC VARSPLIC CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD METAL ACT\_SITE DOMAIN AJ130826; CAB46528.1; -. AJ130827; CAB46529.1; -. D63795; BAA09864.1; -. P08473; 1DMT. PR00786; 599 600 603 659 663 158 \_ Alternative NEPRILYSIN 762 599 600 603 663 158 179 202 202 202 308 375 531 624 81 Peptidase\_M13. splicing. SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). MGSLRPPQGLGLQWSSFFLGKKGPGLTVSLPLLASS RTVWPPLRAALAALGMSSYKRATLDEEDLVDSLSEGDVYPN N-LINKED (GLCNAC. . .) (POTENTIAL).
MGSLRPPQGLGLOWSSFFLGKKGPGLTVSLPLLASS -> N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED PROTON BY SIMILARITY ZINC (CATALYTIC) (POTENTIAL) MSSYKRATLDEEDLVDSLSEGDVYPNG (IN ISOFORM B) (CATALYTIC) DONOR (BY SIMILARITY) (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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MGSLRPPQGLGLQWSSFFLGKKGPGLTVSLPLLASS

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RESULT 10
ECE1_BOVIN
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                                                           P42891,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                            Bos taurus (Bovine).
                                                                                                                                                                 ECE1_BOVIN
                                                                                                                                                                                                                                                  745 FRCPLGSPMN-PRHKCEVW 762
                                                                                                                                                                                                                                                                                   731 FNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                           630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 LEIKKAFEESI-STLKWMDEDTRRSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 MNETRIEELRAKPLMELIEKLG-GWNI-----TGPWAKDNFQ--DTLQVVTAHYRTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 MNEKAIEKADAKPILHILRHSPFRWPVLESNIGPEGVWSERKFSLLOTLATFRGQYSNSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 YACGGWIKANPYPDGHSRWGTFSNLWEHNQAIIKHLLENSTASA--SEAEKKAQYYYRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                  FKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENTADNGGLREAFRAYRKWINDRRQGLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWNSTESEEK
                                                                                                                                                                                                                                                                                                            - ILPTLGLTSNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLSNSKEFSEH
                                                                                                                                                                                                                                                                                                                                         PLLPGITFTUNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKA 730
                                                                                                                                                                                                                                                                                                                                                                             FKQQTECMVQQYNNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             DL-----YFENAMRFFNFSLRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKNIASEII 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I----FYP--VEINESEPIVVYDKEYLRQVSTLINSTDKCLLNNYMMWNLVRKTSSFLDQ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDEDSIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPFLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFSVYVSADSKNSNSVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLL-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVVLV-TLLAAGLVACLAALGIQYRTRTPPVCLTEACVSVTSSILNSMDPTVDPCQDFFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.4%; Score 1243.5; I
37.5%; Pred. No. 4.6e-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129; Mismatches 284; Indels 49;
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLRESVLHLALQMSSYKRATLDEEDLVDSLSEGDVYPNG
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                                                                                                                                                              754 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 762;
   Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570
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CARBOHYD
170 MNETRIEELKAKPLMELIEKLG-GWNI-----TGPWDKDNFQ--DTLQVVTSHYHTSP
                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                  143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV
                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01431; Peptidase Mi3; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                  112 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M13.002; ... InterPro; IPR000718; Peptidase_M13. InterPro; IPR000130; Zn_Mrpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z35306; CAA84547.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 83 FACDGWISNNPIPEDMPSYGVYFWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
                                                                                                                                     53 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P08473; 1DMT.
                                                                                                                                                                     23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt M., Kroeger B., Jacob E., Seulberger H., Subkowski T., Otter R., Meyer T., Schmalzing G., Hillen H.;
"Molecular characterization of human and boyine endothelin converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-95104423; PubMed-7805846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; NCBI_TaxID=9913;
                                                                                                                                                                                                                                      Pocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gnal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.
CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the
Trp-1-Val-22 bond in the precursor.
ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lett. 356:238-243(1994).
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                   367
523
616
635
754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metalloprotease; Zinc; Glycoprotein; Transmembrane,
                                                                                                                                                                                                              Conservative 120; Mismatches
                                                                                                                                                                                                                                                                                                                                   754
592
592
595
651
655
150
171
171
194
254
300
346
346
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                                                                                                                                                                                                                                                                                   85616 MW;
                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                               Score 1241.5;
Pred. No. 6.2
                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .
                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY SIMILAR ZINC (CATALYTIC) (BY SIMILAR PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                               E9276CCCB8E6FF4C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .
                                                                                                                                                                                                                               .2e-76
                                                                                                                                                                                                           282; Indels
                                                                                                                                                                                                                                             DB 1; Length 754;
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(BY SIMILARITY).
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(POTENTIAL)

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61;

Gaps

21;

169

(POTENTIAL)

(POTENTIAL)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECE2_HUMAN STANDARD; PRT; /8/ AA.

060344; Q96NX4; Q96NX3;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMYYSRIPNLSR 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GAEDTIRPOMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes."
The complete sequences of 100 new cDNA clones from brain which cacode for large proteins in vitro.";
DNA Res. 5:31-39(1998).
DNA Res. 5:31-39(1998).
THE THACTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
LOTENZO M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,
Marsden P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 TNOIREPAGELOKPEFWGTEYPRSLSYGAIGVIVGHEFTHGEDNNGRKYDKNGNLDPWWS 604
                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                   species and chromosomal
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                     "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA
                                                                                                                                                         MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DL-----YFENAMRF-----FNESWRYTADQLRKAPNRDQWSMTPPMVNAYYSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM-----NDTHVNE 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQUADEKEMEVNYGTKKTCLPRWKECVSDTENTLGFALGPNEVKATFAEDSKNIASEII 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TESEEKFKEKTKCMINOYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEFSEHFHCPPGSPMN-PHHKCEVW 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQGLEEPLLPGITFTUNQLFFLSYAHVRCUSYRPEAAREQVQIGAHSPPQFRVUGAISUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K
                                                                                                                                                                                                                                                                                                                                                                                                                                             OR KIAA0604
                                                                                                                                                                                                                                  Biophys. Acta 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                       localization."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor;
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       183 RKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
                                    187 NSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI-----EKIGGWNITGPWDQ
                                                             126 RRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP---EGVWSE 182
                                                                                                                                                                          10 ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECIEAAAA 65
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                                                                                                                                                                                                                        Local
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                                                                                                                                                  QKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCLTEACIRVAGK 127
                                                                                          ILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAILKHLLENT-TF 186
                                                                                                                     ILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISR 125
                                                                                                                                                                                                         264; Conservative
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                  787 AA;
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                             144; Mismatches
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                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                       Score 1221;
                                                                                                                                                                                                                                                                                 AGERDPWTVSSEGVHTVDQVLSE -> MNVALQELGAGSN (IN ISOFORM ECE-2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                    MQARHAHVPQLRWETMDVRKLDFPSASFDVVLEKGTLDALL
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                                                                                                                                                                                                                                                                                                              MQARHAHVPQLRWETMDVRKLDFPSASFDVVLEKGTLDALL
                                                                                                                                                                                                                                                                                                                                                       AGERDPWTVSSEGVHTVDQVLS -> MNVALQELGAGSNMV
                                                                                                                                                                                                                                                                                                                                         EYKRATLRDEDAPETPVEGGASPDAM (IN ISOFORM
                                                                                                                                                                                                                                                                     CC2D2B0F0EBF7239 CRC64;
                                                                                                                                                                                                                               1.6e-74
                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                           Length 787;
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RESULT 12
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                        5.5. INACTIVE AT NEUTRAL PH.

-!- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
Trp-|-Val-22 bond in the precursor.
-!- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
                                                                                                                                                                                sensitive metalloprotease with acidic pH optimum."
                                                                                                                                                        J. Biol. Chem. 270:15262-15268(1995).
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                01-OCT 1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
                                                                                                                                                                                                                      Emoto N.,
                                                                                                                                                                                                                          MEDLINE=95318093; PubMed=7797512;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                          Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon
                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                             ECE2_BOVIN
Q10711;
                                                                                                                                                                                                                                                                     NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                         BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 LSNSRDFLRHFGCPVGSPMNPG-QLCEVW 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 MFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
                     European Bioinformatics Institute.
                                                                  SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Type II membrane protein.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 IANYLWRMYYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 DNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYL-NRTAN 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKADAIYDMIGFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISELQALAPSMDWLEFLSF1LSP-----LELSDSEPVVVYGMDYLQQVSELINRTEPSI 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISELSAMIPQFDWLGYIKKVIDTRLYFHLKDISPSENVVVRVPQYFKDLFRILGSERKKT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMS
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             non-profit
                                                                                                                                                                                                               Yanagisawa M.;
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         institutions as long
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There are no restrictions on ong as its content is in no
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476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT
                                      462 FALGSLFVKATFDRQSKEIAEGMISEIRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM
                                                                            416 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
                                                                                                                  402 TEPSVLNNYLIWNLYQKTTSSLDHRFESAQEKLLETLYGTKKSCTPRWQTCISNTDDALG 461
                                                                                                                                                                                                                                                                                                                                                                                  178 GVWSERKESLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                      183 NT-TFNSSSEAERKTQRFYLSCLQVERIEELGA----HALRD-----LIDKIGGWNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KSISRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG---PE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 RVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNNSNSLWDQNQAILKHLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000718; Peptidase_M13.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQVHRDPSHSTCLTEACI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ETGSSVETGKKANRGTRIALYVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECI 60
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                                                                                                                                                      ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415
                                                                                                                                                                                            YHKMSIAELQALAPSMDWLEFLSFLLSP-----LELGDSEPVVVYGTDYLQQVSELINR 401
                                                                                                                                                                                                                                  YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS
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                                                                                                                                                                                                                                                                                                                                              GPWDQDNF--MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL- 287
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787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F085C2921DAF0BF2 CRC64;
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4.9e-72;
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   (See http://www.isb-sib.ch/announce/
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Damage-induced neuronal endopeptidase)
ECEL1 OR XCE OR DINE.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                581 TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JMI0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656 AYRKWINDRRQGLEEPLLPGITFTUNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 EGNLRPWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metallopeptidase expressed in response to neuronal damage and activates superoxide scavengers."

Proc. Natl. Acad. Sci. U.S.A. 97.4345-4350(2000).

1- FUNCTION: May contribute to the degradation of peptide hormones involved in the inactivation of neuronal peptides.

1- COPACTOR: Binds 1 zinc ion (By similarity).

1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).

1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kiryu Seo S., Sasaki M., Yokohama H., Nakagomi S., Hirayama T., Aoki S., Wada K., Kiyama H.; Madage-induced neuronal endopeptidase (DINE) is a unique metallopeptidase expressed in response to neuronal damage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                     MEROPS; M13.007;
MGD; MGI:1343461; Ecell.
Interpro; IPR000718; Peptidase_M13.
Interpro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB026294; BAA95005.1; -. HSSP; P08473; 1DMT.
                               DOMAIN
                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                       PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                          TRANSMEM
                                                                                                                                                        lycoprotein; Transmembrane;
                                                                                                                                                                                                                                                         PR00786; NEPRILYSIN
                                                                                                                                                                                           Protease; Metalloprotease; Metal-binding; Zinc;
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                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                             (POTENTIAL).
LUMENAL (POTENTIAL)
                                                                                                                                                                         Signal-anchor
             (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 HILKLDOATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 ------GGWDLGGAADRPGAARWDLNRLLYKAQGVYSAAALFSLTVSLDDRNSSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 WPVLESNIGPEGVW------SERKFSLLQTLATERGQYSNSVFIRLYVSPDDKASNE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 EERLRRLL-----ARPTGGPGGAAORKVRAFFRSCLDMREIERLGPRPMLEVIEDC--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 SGRSAS-GSRSGLPRWNRREVCLLSG-LVFAAGLCAILAAMLALKYLGPGAAGGGGACPE 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 YCLKPECIEAAAAILS-KVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 PSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 GCPERKAFARAARFLSANLDASIDPCQDFYSFACGGWLRRHAIPDDKLTYGTIAAIGEQN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Госат
                                                                                                                                                                                                                                                                                                                                                                                                                                        483 QRLE-ELDWIDAQTKAAARAKLQYMVVVGYPDFLLKPEAVDKEYE-FEVHEKTYFKNIL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395
Q9JHL3; Q9Z192;
                                                                                                                                                                                                                                                                                                                                                                        541 NSIRESIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQMVYPAGILQ-PTLYDPDFPQ 599
                                                                                                                                                                                                                                                                                                                                                                                                         508 QTRKYLAQSDEFWLRKAVPKTEWETNPTTVNAFYSASTNQIREPAGELQKPEFWGTEYPR 567
                                                                                                                                                                                                                                                                      626 YWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
                    ECEL_RAT
                                                                                                                                                                     713 IAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGSVSQFEEFGRAFHCPKDSPMN-PVHK 771
                                                                                                                                                                                                    686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
                                                                                                                                                                                                                                       660 YNOR----VNGKHTLGENIADMGGLKLAYYAYQKWV--REHGPEHP-LHRLKYTHNOLFF
                                                                                                                                      746 CRLW 749
                                                                                                      772 CSVW 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIKIAEIMIPHEN---RTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDIS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GN-----DKPQELARVCLGQANRHFGMALGALFVHEHFSAASKAKVQQLVEDIKYILG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEEEVVLLATDYMOOVSOLIRSTPRRILHNYLVWRVVVVLSEHLSSPFREALHELAKEME 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTLLPQWDK-----CVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFI 447
                                                                                                                                                                                                                                                                                                         SLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWWTEASYSRFLHKAECIVRLYDNETV 659
                                                                                                                                                                                                                                                                                                                                        SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWNSTESEEKFKEKTKCMINQYSNY-- 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 159; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
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87993 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%; Score 992; DB 1; 30.7%; Pred. No. 3.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
, 53A4595D7C5F34B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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CARBOHYD
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METAL
                                   CARBOHYD
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                                                                                           ACT_SITE
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                                                                                                                                                                                                                                   InterPro; IPR000718; Peptidase_M13.
InterPro; IPR000130; zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                 EMBL; AB026293; BAA95004.1; --
EMBL; AB023896; BAA95006.1; --
EMBL; Y16188; CAA76114.1; --
HSSP; P08473; IDMT.
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            PROSITE; PS00142; ZINC_
                                                                                                                                                                                                                                                                                          MEROPS; M13.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endopeptidase family, is preferentially expressed in the CNS.", Brain Res. Mol. Brain Res. 64:211-221(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A., "XCE, a new member of the endothelin-converting enzyme an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 431-632 FROM N.A. MEDLINE-99132387; PubMed-9931490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Damage-induced neuronal endopeptidase (DINE) is a unique metallopeptidase expressed in response to neuronal damage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activates superoxide scavengers.";
Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Wistar; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiryu-Seo S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20226106; PubMed-10759559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)
                                                                                                                                                                                  coprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Damage induced neuronal endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protect against C2-ceramide-induced apoptosis.

COFACTOR: Binds 1 zinc ion (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein.

TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in nucleus of the thalamus part of the hypothalamus, in cranial spinal tract trigeminal nucleus. Not detected in cerebral cortex, remaining and cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: By mechanical damage to nerve cells. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May contribute to the degradation of peptide hormones and be involved in the inactivation of neuronal peptides. Cleave the synthetic substrate 2-Gly-Gly-Leu-pNA and releases pNA, May
                                                                                                                                                                   Protease; Metalloprotease; Metal-binding; Zinc;
in; Transmembrane; Signal-anchor.
                               83
612
613
616
672
255
322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Sasaki M., Yokohama H., Nakagomi S., Hiyama T.,
                                                                                                                                                                                                        _PROTEASE; 1
        ZINC (CAT)
ZINC (CAT)
N-LINKED
N-LINKED
N-LINKED
                                                                                 BY SIMILARITY.
                                                                                    ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                           LUMENAL (POTENTIAL)
                                                                                                                             (POTENTIAL)
                                          (CATALYTIC) (BY SIMILARITY). (CATALYTIC) (BY SIMILARITY).
        (GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL)
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ECEL_HUMAN STANDARD; PRT; 775 AA.
095672; O9NY95;
15-UN-2002 (Rel. 41, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein).
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                                                                                                                                                                                     772 CSVW 775
                                                                                                                                                                                                                   746 CRLW 749
                                                                                                                                                                                                                               713 IAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGSVSQFEEFGRAFHCPKDSPMN-PVHK 771
                                                                                                                                                                                                                                                            686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS
                                                                                                                                                                                                                                                                                                                           626 YWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
                                                                                                                                                                                                                                                                                                                                                                                          568 SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESBEKFKEKTKCMINQYSNY--
                                                                                                                                                                                                                                                                                                                                                                                                                         541 NSIRFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQMVFPAGILQ-PTLYDPDFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 DMLEKENEWNDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 GN-----DKPQELARVCLGQANRHFGMALGALFVHEHFSAASKAKVQQLVEDIKYILG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 EEEEVVLLATDYMQQVSQLIRSTPRRILHNYLVWRVVVVLSEHLSDPFREALHELAKEME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 PSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRWYYSRIPNLSRRFQYRWLEFSRVIQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 EIKIAEIMIPHEN----RTSEAMYNKMNISELSAMIPOFDWLGYIKKVIDTRLYPHLKDIS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 YVIRIDQDGLTLPERTLYLAQDEGSEKVLAAYKVFMERLLRLLGADA--VEQKAQEILQL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 HILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 WPVLESNIGPEGVW------SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 DLKLKELLEKSISRRRDT-----EAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 GCPERKAFARÁRFLSANLDASIDPCQDFYSFÁCGGWLRRHAIPDDKLTYGTIAAIGEQN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 YCLKPECIEAAAAILS-KVNLSVDPCDNEFRFACDGWISNNBIPEDMPSYGVYPWLRHNV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 SGRSAS-GARSGLPRWNRREVCLLSG-LVFAAGLCAILAAMLALKYLGPGAAGTGGACPE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 TGKKANRGTRIAL------VVFVGGTLVLGTILFLVSQGLLSLQ------AKOE 52
                                                                                                                                                                                                                                                                                            YNOR----VNGKHTLGENIADMGGLKLAYYAYOKWV--REHGPEHP-LHRLKYTHNQLFF
                                                                                                                                                                                                                                                                                                                                                           SLNYGGIGTIIGHELTHGYDDWGGQYDRSGNLLHWWTEASYSRFLHKAECIVRLYDNFTV 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTLLPQWDK-----CVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQRLANISVSEYDDLRRDVSSVYNKVTLGQLQKITPHLQWKWLLDQIFQ-----EDFS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EERLRRLL-----ARPTGGPGGAAQRKVRAFFRSCLDMREIERLGPRPMLEVIEDC--- 209
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775 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 977; DB 1; Length 775; 30.5%; Pred. No. 4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158; Mismatches
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1; 0823091F98A41556
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PARTHER THE TREET TO SOCIO SOC
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MEDLINE-99132387; PubMed=9931490;
Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A.;
Valdenaire of the endothelin-converting enzyme and neutral endopeptidase family, is preferentially expressed in the CNS.";
Brain Res. Mol. Brain Res. 64:211-221(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20164043; PubMed-10698686;
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                                                                                                                                                                                                                                                                                       METAL
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ130734;
HSSP; P08473; 11
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                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
                           CONFLICT
                                                                              VARIANT
                                                                                                                                VARIANT
                                                                                                                                                            CARBOHYD
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putamen, spinal cord, medulla and subthalamic nucleus. A strong signal was also detected in uterine subepithelial cells and around renal blood vessels. Detected at lower levels in amygdala, caudate, thalamus, pancreas and skeletal muscle. Detected at very low levels in substantia nigra, cerebellum, cortex, corpus callosum and hippocampus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: May contribute to the degradation of peptide hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
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IPR001230; Prenyl_site.
IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                protease; Metalloprotease; Metal-binding; Zinc;
ln; Transmembrane; Signal-anchor; Polymorphism.
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                                                                                   /FTId=VAR_012813
                                                                                                                                ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
H -> Q (IN DBSNP: 2741281).
                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                LUMENAL (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                           /FTId=VAR_012814.
V -> I (IN REF. 2
                                                                                H (IN DBSNP:1529874).
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745 LGSVSQFEEFGRVLHCPKVSPMNPA-HKCSVW 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIPOFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVFMERVLSLLGADA--VEQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHEN---RTSEAMYNKMNISELS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLYKAQGVYSAAALFSLTVSLDDRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKVLAAY
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                                                                                                                                                                                                                                              FYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KITPHLRWKWLLDQIFQ------EDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYL 401
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                                                                                                                                        LHWWTEASYSRFLRKAECIVRLYDNFTVYNQR----VNGKHTLGENIADMGGLKLAYHAY
                                                                                                                                                                       DPWWSTESEEKFKEKTKCMINQYSNY--YWKKAGLNVKGKRTLGENIADNGGLREAFRAY
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                                                                   QKWV--REHGPEHP-LPRLKYTHDQLFFTAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRV
                                                                                                                                                                                                                                                                                                                                                                                                                            YWRVYVYLSEHLSPPFREALHELAQEMEGS-----DKPQELARVCLGQANRHFGMALG
                                   NGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                    RKWINDRROGLEEPILPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRV 717
                                                                                                                                                                                                             YYLPNKNQMVFPAGILQ-PTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNL
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775 AA;
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87781 MW;
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Search completed: May 21, 2003, 18:48:18 Job time: 31 secs

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OM protein - protein search, using sw model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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3958
1 MEAETGSSVETGKKANRGTR......AFNCPPNSTMNRGMDSCRLW 749
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1: sp_archea:*
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sp_vertebrate:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 3 3 5 5 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
3819 1375.5 1375.3 1368.5 1361.5 1368.5 1368.5 1368.5 1213.5 123.5 1248.5 1223 1229 1209 1208	Score
34.9 34.9 34.6 34.6 33.7 31.8 31.7 31.5 30.9 30.9	% Query Match Length
742 765 765 765 779 779 770 770 770 772 758 848 848 763 763	ength DB
11 035812 09ERK3 11 09ERK3 11 09CZV6 11 09CZV6 11 09CZV7 11 09ERK2 13 093994 4 096PH9 4 096PH9 6 028616 6 028610 5 09BLH1 5 09BLH1 5 09ERK2 11 092376	BID
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044857 caenorhabdi 09xx01 drosophila 08t60 venturia ca 018673 caenorhabdi 091714 drosophila 091714 drosophila 091720 methanosarc 09a2q2 caulobacter 050642 porphyromon 010831 caenorhabdi 09386 gallus gall 05364 mycobacteri 09361 drosophila 096075 mycobacteri 09pfil xylella fas 090136 drosophila 090430 drosophila 0904569 caenorhabdi 08ws6 dermacentor 09eqf2 mus musculu 09tj6 ancylostoma 08vts9 lactobacill 022763 caenorhabdi 028vts9 lactobacill 022763 caenorhabdi 03vas4 drosophila 08vts9 lactobacill 023763 caenorhabdi 045131 haemonchus 09tj5 ancylostoma	

## ALIGNMENTS

<b>5</b> HO	DR SQ	닯	DR	DR	R F	DR	DR	DR	RĽ	RT	RT	RA	RA	RA	RA	RX	8	RP	RN	OX.	8	8	ွှင်	2 E	뒭	DI C	3 1	2	5 5	035812	RESULT
Query Match 96.5%; Score 3819; DB 11; Length 749; Best Local Similarity 95.3%; Pred. No. 3.1e-256; Matches 714; Conservative 22; Mismatches 13; Indels 0; Gaps	ZINC_PROTEASE; 86305 MW;	PRINTS; PROUVES; NEPRILITSIN: UNKNOWN 1.	Pfam; PF01431; Peptidase_M13; 1.	InterPro; IPR000130; Zn_MTpeptdse.	Interpro; IPR001230; Prenyl_site.		HSSP; P08473; 1DMT.	EMBL; AJ001637; CAA04890.1;	Genome Res. 7:573-585(1997).	dominant hypophosphatemic_rickets.";	"Genomic organization of the human" PEX gene mutated in A inner		Borzym K., Pohl T., Oudet C., Econs M.J., ROWE F.S., Relimator S.,	M., Steffens C., Klages S.,	T.M., Hennig S., Boeddrich A., Lorenz B	5; PubMed=919930;	NCISOR;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=10116;		a; Chordata; Craniata; Vertebrata;	s norvegicus (Rat)	PHEX	_	(TrEMBLrel. 21, Last	05,	OI TANIJOOO (MATURITO) OI (Treated)		BIZ DESTIMINARY: PRT: 749 AA.	TLT 1

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RESULT 2
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ID Q9ERK3
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D7 01-M
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SEQUENCE FROM N.A.
MEDLINE-2123028; PubMed-11278416;
Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya
Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita 1
Iwataubo T., Saido T.C.;
                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neprilysin-like peptidase alpha.
                                                                                                                                                                     MELL1
                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                   Q9ERK3;
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                                                                                                                                                                                                                                                                                                                                         INDRROGLEEPLLPGITFINNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIMNDTHVNEDLKAIKESEADYEGNVLQTRKYLAQSDEFWLRKAVPKTEWETNPTTVNAF 540
                                                                                                                                                                                                                                                                                                                                                                       ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                  INDRRQGVEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIMNDTYVNEDLKAIKFSESDYFGNVLQTRKYLAQSDFFWLKKAVPKTEWFTNPTTVNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFVNVHFQEDKKEMMEELIEGVRWAFIDMLEKENEWMDAGTKRKAQEKARAVLAKVGYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAKSYRDALIKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAKSYRDALYKEMYDTAVLLGANSSRAEHDMKSYLRLEIKIAEINIPHENRTSEAMYNKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST
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                                                                                                                                                                                                                                                             PRELIMINARY;
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               Tomita T.,
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R MEDOPS; M13,008; ...

R MGD; MGI:1351603; Mell1.

R InterPro; IPR000718; Peptidase_M13.

IR InterPro; IPR000130; Prenyl_site.

DR InterPro; IPR000130; Zn_mtpeptdse.

DR Pfam; PF01431; Peptidase_M13; 1.

DR PRINTS; PR00786; NEPRILYSIN.

DR PROSITE; PS00142; PRENYLATION; UNKNOWN_1.

DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

DR PROSITE; PS00142, ZINC_PROTEASE; UNKNOWN_1.
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714 SLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 742
                                                                                                          660 WINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNG
                                        720 AISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                597
                                                                                                                                                                                                                                                                                                                    478
                                                                                                                                                                                                                                                                                                                                      483 M--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF
                                                                                                                                                                                                                                                                                                                                                                             419 IKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKAMNIREQIGYPDYI 477
                                                                                                                                                                                                                                                                                                                                                                                                               423 VDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFI 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 QNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 RFGLKGFNWTLFIQNVLSSYEVELF-----PDEEVVVYGIPYLENLEDIIDSYSARTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 ANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMF 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
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J. Biol. Chem. 276:21895-21901(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
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                                                                        WLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLG
                                                                                                                                                DWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLR
                                                                                                                                                                                      PWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLREAFRAYRK
                                                                                                                                                                                                                                                                                                  LEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAF
                                                                                                                                                                                                                          YSPNRNQIVEPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNML 596
                                                                                                                                                                                                                                                              YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-VRKAYLEFMT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK-----WNETMGLKWELERQLAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSLLQTLATF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR--PAVEKAKT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLMVLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%; Score 1380; DB 11; Length 742; 38.8%; Pred. No. 3.6e-87;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Neprilysin-like metallopeptidase 1 (Neprilysin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghaddar G., Ruchon A.F., Carpentier M., Marcinkiewicz M., Seidah N.G., Crine P., DesGroseillers L., Boileau G.;
"Molecular cloning and biochemical characterization of a new mouse testis soluble zinc-metallopeptidase of the neprilysin family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JLI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of neprilysin-like peptidase cDNAs.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AF136569; AAF69247.1; -
EMBL; AF302076; AAG18447.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10749671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M13.008; -
MGD; MGI:1351603; Mell1.
InterPro; IPR000718; Peptidase_M13
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                                                                                                                                                                                                       FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS
                                                                                                                                                                                                                                       --PAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK-----WNETMGLK
                                                                                                                                                                                                                                                                     DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER----K 184
                                                                                                                                                                                                                                                                                                     ENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR 148
                                                                                                                                                                                                                                                                                                                                    SKYNLSYDPCDNFFRFACDGWISNNPIPEDMPSYGYYPWLRHNVDLKLKELLEKSISRRR 127
                                                                                                                                                                                                                                                                                                                                                                  GAIVTLGVFYSIGKQLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88
                                                                                                                                                                                                                                                                                                                                                                                                GTRIALVVF--VGGTLVLGTILF-----LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
                                                                                                            VRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY
                                                                                                                                          YRDALYKFMYDTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
                                                                                                                                                                          WELERQLAVINSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-
             ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES
                                             HRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELF-----PDEEVVVYGIPYLENLED
                                                                           NKMNISELSAM--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00294; PRENYLATION; UNKNOWN_1
PS00142; ZINC_PROTEASE; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                765 AA; 88699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347:419-429(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 38.8%; Pred. No. 7.7e Conservative 147; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1DMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saido T.C.;
34.8%; Score 1375.5; DB 11; Length 765; 38.8%; Pred. No. 7.7e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D3662F1CE5B957F7 CRC64;
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Best Local
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Q9QZV6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yokoyama M., Matsuo M.; "Molecular identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1351603; Mell1.
InterPro; IPR000718; Peptidase_M13.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF157106; AAF13153.1;
HSSP; P08473; 1DMT.
MEROPS; M13.008; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variety of vascactive peptides.";
J. Biol. Chem. 274.33469-33477(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20011457; PubMed=10542292; Ikeda K., Emoto N., Raharjo S.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 IIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS 431
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 742 AA; 85945 MW; CF5FF9D982471157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00786; NEPRILYSIN.
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78 DNFFRFACDGWISNNPIPEDMPSYGYYPWLRHNYDLKLKELLEKSISRRRDTEAIQKAKI 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRQAYKAYLRWLAD----GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV 726
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                                                                                                                                GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPC
                                                                     GLMYLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC
                                                                                                                                                                                                                                     similarity
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                         34.7%;
38.7%;
                                                                                                                                                                                                             149; Mismatches
                                                                                                                                                                                                   Pred. No. 1.1e-86;
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ENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR--PAVEKAKT 133

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RESULT
Q9QZV7
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Q9QZV7;
01-MAY-2000
MGD; MGI:1351603; Mell1.
InterPro; IPR000718; Peptidase_M13.
                                                                                  metalloprotease, the soluble secreted form of which variety of vasoactive peptides.";
J. Biol. Chem. 274:32469-32477(1999).
                                                                                                                                                                                                                                                                                                                             MELL1
                                                                                                                                    Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
Yokoyama M., Matsuo M.,
"Molecular identification and characterization of novel membrane-bound
                                          MEROPS; M13.008; -.
                                                        EMBL; AF157105; AAF13152.1; HSSP; P08473; 1DMT.
                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20011457; PubMed=10542292;
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                          Soluble secreted endopeptidase.
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                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---KFSLLQTLATF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWWSTESEEKFKEKTKCMINOYSNYYWKKA-GLNVKGKRTLGENIADNGGLREAFRAYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYKAYLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANYLVWRMVYSRIPNISRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMF 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFGLKGFNWTLFIQNVLSSVEVELF-----PDEEVVVYGIPYLENLEDIIDSYSARTM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQFTLGMPSREYYFQEDNNHK-VRKAYPEFMT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV
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BUTTO

Q9ERK2; Q9ERK2

PRELIMINARY;

PRT;

779 A

01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation updat
Neprilysin-like peptidase gamma.

gamma.

Last annotation update)

Q9ERK2 RESULT 6

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Best Local
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; MEDRILYSIN.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 765 AA; 88651 MW; 567D3C17764C0F3F CRC64;
          727
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                                                                                                                                                                                                                                                                                                                                                                                                                         413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 NKMNISELSAM--IPQFDWLGYIKKY---IDTRLYPHLKDISPSENVYVRVPQYFKDLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 VRKAYPEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 GAIVTLGVFYSIGKQLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GTRIALVVF--VGGTLVLGTILF-----LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loca.
HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 765
                                    HSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                     VRQAYKAYLRWLAD----GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
                                                                                                  LREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGA
                                                                                                                                                 RNFDKNGNMLDWWSNFSARHFQQQSQCMTYQYGNFSWELADNQNVNGFSSLGENIADNGG
                                                                                                                                                                                      RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGG
                                                                                                                                                                                                                               IIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNG
                                                                                                                                                                                                                                                       FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG
                                                                                                                                                                                                                                                                                                        REQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLW
                                                                                                                                                                                                                                                                                                                                               LAKVGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIDSYSARTMONYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVALDK-----WNETMGLK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 34.6%; Score 1368.5; Similarity 38.7%; Pred. No. 2.3e
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endopeptidases.";
J. Biol. Chem. 276:21895-21901(2001).
EMBL, AF302077; AAG18448.1; -.
HSSP; P08473; IDMT.
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 779 AA; 89709 MW; 5E48CA530828584B CRC64;
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 LYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER----KFSLLQTLATF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                   246 SVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQE 305
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                                                                                                                                                                                419 RYDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSV 478
                                                                                                                                           446 FIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM--NDTHVNEDLKAIKFSEADYF 503
564 EYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWNSTESEEKFKEKTKCMINQYS 623
                                                                     504 GNYLOTRKYLAQSDEFWLRKAVPKTEWETNPTTVNAFYSASTNQIRFPAGELQKPFFWGT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIOKAKI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLMVLLLLLLGAIVTLGV---FYSIALRDSSLKSDICTTPSCVIAAARILENMDQSRNPC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK-VRKAYLEFMT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYRSCMNOSVIEKRDSEPLLSVLK-MYGGWPVAMDK-----WNETMGLKWELERQLAVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMYNKMNISELSA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMV 254
                                                                                                                                                                                                                   WLEFSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWA 445
                                                                                                                                                                                                                                                                                          LYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYR 385
                                                                                                                                                                                                                                                      LF----PDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEA 418
                                                                                                                                                                                                                                                                                                                             RFGLKDRVSLCSPGCPGTHSVDQAGLELGNPPASDSRVLGLKGFNWTLFIQNVLSSVEVE 365
                                    ENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SK 596
                                                                                                          FYDNLDELN-WADEESKKKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYF 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                    Conservative 148;
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37.0%; Pred. No. 7.3e
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perca flavescens (Yellow perch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Langenau D.M., Goetz F.W., Roberts S.B.;
"The upregulation of messenger ribonucleic acids during 17alpha,
20beta-dihydroxy-4-pregnen-3-one-induced ovulation in the perch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773 MKRCRIW 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 LFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRG 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99445407; PubMed=10514552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percidae; Perca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Endocrinol. 23:137-152(1999).
EMBL; AF077612; AAC28366.1; -.
HSSP; P08473; IDMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8167;
                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.
SEQUENCE 770 AA; 88135 MW; D29F216CBC
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000718; Peptidase_M13.
InterPro; IPR001230; PrenyL_site.
InterPro; IPR0011230; Pr.mypeptdse.
InterPro; IPR000130; Zn.mypeptdse.
Pfam; PF01431; Peptidase_M13; 1.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00786; NEPRILYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M13.001;
                                                                                                                                  116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVL----E 171
                                                                172 SNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQAT-LSLA 230
231 VREDYLDNSTEAKSYRDALYKFMVDTAVLL----GANSSRAE--HDMKSVLRLEIKIAEI 284
                                 196 TNYG-----KTWRLEDVIAKLNEKYGTQLLVNFFVGTDDRDSNSYIIHFDQQTNLGLL 248
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 TGDCTQSASRLIENMDDSVDPCDNFYQYACGGWLKKNIIPETSSRYSTFDILRDELEVIL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYYWKKA-GLNYKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQ 682
                                                                                                                                                                                                                                                                  3 AETGS--SVETG--KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQ---EYCL 55
                                                                                                                                                                                                                                    AEAGDLRMMETNPPKSAKKPRWTSLEV---GLTTIVSLLEIVIVALIILFATOKTDEICT 78
                                                                                                  KGYLEK---TDEGEATLSTRAKTLYKSCTNESLIELRGGAPLLDML-PDVFEWPVAVDNWE 195
                                                                                                                                                                                                  KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                        33.7%; Score 1335; 38.0%; Pred. No. 56
                                                                                                                                                                                                                                                                                                           146; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                               D29F216CB041BACC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                 No. 5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       770 AA
                                                                                                                                                                                                                                                                                                                                               DB 13; Length 770;
                                                                                                                                                                                                                                                                                                                 283; Indels 50;
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                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                         PROSITE; PS00294; PRENYLÄTION; UNKNOWN 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SEQUENCE 770 AA; 88523 MW; DF9C08F4AA59
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000718; Peptidase_M13.
InterPro; IPR0001230; Prenyl_site.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of MMEL2, a gene coding for a novel human member of the neutral endopeptidase-24.11 family."; DNA Cell Biol. 20:493-498(2001). EMBL; AF336981; AAL08942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonvouloir N., Lemieux N., Crine P., Boileau G., DesGroseillers L.; "Molecular cloning, tissue distribution, and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neprilysin-like metallopeptidase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96РН9;
Q96РН9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M13.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-21444797; PubMed-11560781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
68 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                        42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697 RPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 NNTLGENIADNGGIRQAYQAYKNYV--EKHG-EEPSLPGINLSHNQLFFLNFAQVWCGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           637 KRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSY 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 VGHEFTHGFDNNGRKYDKNGNLDDWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 FFWLRKAVPKTEWETNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVI 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 LRKLRVKVNKEEWYTGAAVVNAFYSSSKNQIVFPAGILQPPFF-SKGQAKSLNYGGIGMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 NVVVRVPQYEKDLFRILGSERKKTIANYLYWRMVYSRIPNLSRRFQYRWLEFSRVIQGTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 KVINYSPNYYRRLNLILARYNKRDLQNYMYWRFAMNMYVGLSRSYRDTRKAFRKALSGTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGHEITHGFDDNGRNYDKDGDLKDWWTPGSTDRFLDLSKCIVNQYGNFSWDLANGLHLNG
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                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIPHENRTSEA-MYNKMNISELSAMI-----PQFDWLGYIKKVIDTRLYPHLKDISBSE 337
                                                                                                                                        Conservative 145; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                               33.7%; Score 1332.5; DB 39.2%; Pred. No. 7.4e-84;
                                                                                                                                                                                                                                                         DF9C08F4AA56A23B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 AA.
                                                                                                                                                                                       DB 4; Length 770;
                                                                                                                           258; Indels
                                                                                                                              37;
                                                                                                                           Gaps
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RESULT 9
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Development 127:3523-3532(2000).
                                                                                      Takebayashi-Suzuki K., Yanagisawa M., Gourdie R.G., Kanzawa N.,
                                                 coexpression
                                                      "In vivo induction of cardiac Purkinje fiber differentiation
                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-20363660; PubMed-10903177;
                                                                                                                                                                                                                   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                    Endothelin converting enzyme-1.
                                                                                                                                                                                                                                                                                                                                01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR 2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9DGN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DGN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767 CRVW 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     746 CRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 LQNLKYGAQRSLRKLREKYDPNLWIIGAAYVNAFYSPNRNQIYFDAGILQPPFF-SKEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----- 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPOFDWLGYIKKVIDTRLYPH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 HSPFRWPVLESNIGPEGVWSER----KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GYYPMIRHNYDIKIKEILEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCHNQSVIEKRGSQPLLDIL- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITETNNQLEF 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLL--GANSSR----AEHDMK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVVGGWPVAMDR-----WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 238
                           of preproendothelin-1 and endothelin converting enzyme-
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR000130; Zn_MTpeptdse.
pfam; PF011431; Peptidase_M13; 1.
pRINTS; PR00786; NEPRILYSIN.
pROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 752 AA; 84985 MW; 3B6B3DB7BF900656 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF230274; AAF98287.1; -. HSSP; P08473; 1DMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M13.002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IALVVFVGGTLVLGTILFLVSQGLLSLQAK-QEYCLKPECIEAAAAILSKVNLSVDPCDN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 GMFLGGTDEESTRQQMQQILEFETALANITIPQEKHRDEEVIYHKMTAGELKDLAPAVDW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 VAVLAAVLGACLLGLV------LQYRARPPAVCLSEACISVTSSILSSLDRTVNPCED 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 MMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLK 493
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 --VENDYDAVSDLYFENVMQFYNFSARVTADQLRKPPNRDQWSMTPPTVNAYYSPTKNEI 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 AIKESEAD-----YEGNVLQTRKYLAQSDEFWLRKAVPKTEWETNPTTVNAFYSASTNQI 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 VAEENTAEIKTAFEESLE-TLOWNDEETRKSAKEKADAIYNMIGYPKFILDSKELDK--- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pocar
                                                              028868
                                      Q28868;
                                                                                                                                                                                                                                     673 EEETLPTLGLINHOLFFYGFAQVWCSVRTPESSHEGLITDPHSPSRFRYIGTVSNSWEFA 732
                                                                                                                                                                                                                                                                          669 EEPLLPGITFTUNGLFFLSYAHVRCUSYRPEAAREQVQIGAHSPPQFRVUGAISUSEEFQ 728
                                                                                                                                                                                                                                                                                                                  618 EAFKROTACHVEQYSNYTIN--GEAVNGKHTLGENIADNGGLKAAYRAYQNWL--RKNG-
                                                                                                                                                        733 EHFSCPLGSPMN-PPKKCEVW 752
                                                                                                                                                                                                 729 KAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QACMNESKIEELRAAPLMELI------AKLGGWNITGPWAGGDFN--ATLREVTA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP---EGVWSERKFSLLQTLATFRG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYRISPFFSVYVSADSKNSNYIQVDQSGLGLPSRDYYL-NKTENEKVLAGYLNYMVQL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPELDQREQDAEEKFMEVMYGTKKTCLPRWKFCISDTDNNLGFALGAMFVKATFAEDSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPNLSRREQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMEVDVYFQEDKKE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPFLSTV----FYP--VELNESEPVVVYAKEYLEQVSDLILATDKCLLNNYMIWNLVRKT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVLLGANSSRA-EHDMKSVLRLEIKIAEIMIPHE-NRTSEAMYNKMNISELSAMIPQFDW 314
                                                                                                                                                                                                                                                                                                                                                         EKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRROGL 668
                                                                                                                                                                                                                                                                                                                                                                                                  REPAGELQKEFFWGTEYERSLSYGAIGVIVGHEETHGEDNNGRKYDKNGNLDEWWSTESE 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.8%; Score 1257; DB 13; Length 752; illarity 37.5%; Pred. No. 1.2e-78; Conservative 138; Mismatches 271; Indels 54
                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikura T., Sawamura T., Shiraki T., Hosokawa H., Kido T., Hoshikawa H., Shimada K., Tanzawa K., Kobayashi S., Miwa S., et al; "cDNA cloning and expression of bovine endothelin converting enzyme."; Blochem. Biophys. Res. Commun. 203:1417-1422(1994).
EMBL; 573774; AAB32062.1; EMBL; 573774; AB32062.1; HSSP; P08473; 1DMT.
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Interpro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PR00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 758 AA; 85648 MW; 6A7EA96566BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 MNEKATEKADAKPILHILRHSPFRWPVLESNIGPEGVWSERKFSILQTLATFRGQYSNSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 YACGGWIKANPYPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SYSEAERKAQVYYRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 MNETRIEELKAKPLMELIEKLG-GWNI-----TGPWDKDNFQ--DTLQVVTSHYHTSP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLLGA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                   381 REQYRWLEESRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMEVDVYFQEDKKEMMEELV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 -LNTIFYP--VEINESEPIVIYDKEYLSKYSTLINSTDKCLLNNYMIWNLYRKTSSELDQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF--- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRDTEAIOKAKILYSSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDDCQDFFT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 Match 31.7%; Score 1253.5; DB 6; Length 758; Local Similarity 38.0%; Pred. No. 2.2e-78; Local Similarity 121; Mismatches 280; Indels 61; Les 283; Conservative 121; Mismatches 280; Indels 61;
                                                                                                                                                                                                                                                                                                             457 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFINDPKELDKVFNDYTAVP 515
                                                                                                                                                                                                                                                                                                                                                    440 EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM-----NDTHVNE 490
                                                                                                                                                                                                                                                                     491 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSAS 544
665 RQGLEEPILPGITETUNQLEFLSYAHVRCNSYRPEAAREQVQIGAHSPPQERVNGAISNS 724
                                                                                                                                                                                                                             516 DL-----YFENAMRE-----FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560
                                                               620 NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K 675
                                                                                                       605 TESEEKFKEXTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
                                                                                                                                                 545 TNQIREPAGELOKPEFWGTEYPRSLSYGAIGVIVGHEFTHGEDNNGRKYDKNGNLDPWWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282
                                                                                                                                                                                                                                                                                                                                                                                              RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456
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381 RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
                                                 340 -LNTIFYP--VEINESEPIVIYDKEYLSKYSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 396
                                                                                321 VIDTRLYPHLKDISPSENVYVRVPQYFKDLFRILGSERKKTIANYLVWRMYYSRIPNLSR 380
                                                                                                              283 GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAABLQTLAPAINWLPF--- 339
                                                                                                                                                                                                            203 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLLGA 262
                                                                                                                                                                                                                                           174 MNETRIEELKAKPLMELIEKLG-GWNI-----TGPWDKDNEQ--DTLQVVTSHYHTSP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO00718; Peptidase_M13.
InterPro; IPRO00130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 758 AA; 85620 MW; 39DCB7020999
                                                                                                                                                                                                                                                                         143 MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
                                                                                                                                                                                                                                                                                                      116 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; M13.002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteolytic activation of big endothelin-1."; Cell 78:473-485(1994).
                                                                                                                                                                                                                                                                                                                                   83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIOKAKILYSSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanagisawa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ECE-1: a membrane-bound metalloprotease that catalyzes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu D., Emoto N., Giaid A., Slaughter C., Kaw S., deWit D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94340737; PubMed=8062389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q28010;
                                                                                                                                                                                                                                                                                                                                                                    57 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEGCISVTSSILSSMDPTVDPCQDFFT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelin converting enzyme-la.
                                                                                                                                                                                                                                                                                                                                                                                                  23 LVVFVGGTLVLGTILFLVSOGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNEFR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  735 KEFSEHFHCPPGSPMN-PHHKCEVW 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 KNGAEQ-TLPTLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNS 734
                                                                                                                                             NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
                                                                                                                                                                             FFSVYVSADSKNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                     282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.5%; Score 1248.5; DB 6; Length 758; 37.9%; Pred. No. 4.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39DCB702099F40A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0786; NEBRILYSIN.
PRINTS; PR01651; SECGEXPORT.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 787 AA; 88171 MW; 3D91D1485CEK
122 SISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSDFRWPVLESNIGPEGVWS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000718; Peptidase M13.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF04431; Peptidase M13; 1.
                                                                                         114 AAARIMSNIDKSVHPCDNEYNFACANWEYDRDIPKDSAALSVLSELGKKVDRQVKLIIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zappulla J.P., Wickham L., Bawab W., Yang X.F., Storozhuk M.V., Castellucci V.F., Descroseillers L., "Cloning and characterization of Apiysia neutral endopeptidase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Neurosci. 19:4280-4292(19)
EMBL; AF104361; AAD51382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuropeptides in Aplysia californica.",
J. Neurosci. 19:4280-4292(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metallo-endopeptidase involved in retract endopeptidase, a neuropeptides in ablvaia california."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99274733; PubMed-10341232;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UA44;
                                                                                                                                                 62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
                                                                                                                                                                                                               68 EPSSGSDGTTSAASGSGGTTSAASGSGGT-----TSADSDGKICVHEGCVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aplysia californica (California sea hare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neutral endopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                              2 EAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   735 KEFSEHFHCPPGSPMN-PHHKCEVW 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 NSSVEAFKQQTACMYEQYGNY--SVNGEPYNGRHTLGENIADNGGLKAAYRAYQNWV--K 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 TESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDR 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 TNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWS 604
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                      Conservative 147; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 1223; 35.6%; Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D91D1485CECE437 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                       3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                      289; Indels 54; Gaps
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RESULT
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                               "Isolation of a 20 hydroxyecdysone inducible nel T endopeptidase 24.11)-like gene and its expressic metamorphosis of Bombyx mori.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ da EMBL, AB048208; BAB33300.1; -.

HSSP: P08473; 1DMT.
                                                                                                                                                                                                                                                                                                             Q9BLH1 PRELIMINARY;
Q9BLH1;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                               Kawasaki H., Zhao X.;
Submitted (SEP-2000)
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyc.
                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                       BMNEP-L.
                                                                                                                                                                                                                                                                                                    Neutral endopeptidase 24.11
                                                                                                                                                                                                                   NCBI_TaxID=7091;
               InterPro;
                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                        VHSPGQYRVIGSLQNSEDFARVFNCPSTSYMN-AANKCQVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFIISKPFVDKFFSPEAKDVALEMISGLQSAFNEIVD-EVEWMDEETKVVAREKNDAIVS
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 473; 1DMT.
IPRO00718; Peptidase_M13.
IPRO01230; Prenyl_site.
IPR000130; Zn_MTpeptdse.
Prenyl_site.
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Best Local (
                                                                    u__JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 97.1 kDa protein.
F18A12.8.
                                                                                                                                                        016796;
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PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.

SEQUENCE 772 AA; 87763 MW; BOD5338EAF4F0D56 CRC64;
                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
                                                                                                                                                                                                                                                     TGFHAPGRFRVIGPMSNMEEFASDFKCPMGSPMNPD-KKCKVW
                                                                                                                                                                                                                                                                         IGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                GGIKEAYYAYQAWTH---RHG-EEARLPGLEKYSPRQLFWLSAANTWCAYYRNEAIKLRIT
                                                                                                                                                                                                                                                                                                                                                                                                         NNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADN
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STRAIN-BRISTOL N2;
Waterston R., Ozersky P., Le T.T.;
Waterston R., Ozersky P., Le T.T.;
"The sequence of C. elegans cosmid F18A12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000718; Peptidase_M13.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF015688; AB66079.2; -.
HSSP; P08473; 1DMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 848 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    None;
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  574 IGVIVGHEFTHGEDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLN
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                                                                                QSREFQKLTKPFDKHEFDISPAVVNAFYSPEKNAITFPAGILQPPFFSGT-FPKAVNYGA
                                                                                                              QS-DFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGA
                                                                                                                                                                                         DWMDEETKAVAIEKANSMINNIGYPDVTNDLPKLDKQYLGLSISDSDTYYYIMKKSVVWM
                                                                                                                                                                                                                       EWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLA
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                                                                                                                                                                                                                                                                                                  GQQQSPPRWKDCAQVPSTVLPLAAGAIYVQAHFQESDKHEALRMIMHLRNSFADLV-RQN
                                                                                                                                                                                                                                                                                                                                                    GTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQQLRVLLEQEVV--TESESINMARATYRSCMNKTQLDELMTGPLFETLTELG-EWPLLQ
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54; Conservative
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Pred. No. 3.
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3.1e-75;
ches 277;
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Best Local
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InterPro; IPR000221; Protamine_P1.
InterPro; IPR000221; Protamine_P1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01431; Peptidase_M13; 1.
PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
PROSITE; PS00048; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 763 AA; 86205 MW; 4B518B0EEF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan H., Mzhavia N., Devi L.A.;
"Mouse Endothelin Converting Enzyme-2 cDNA.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AF396699; AAK83919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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Q923T6;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; M13.003; -
InterPro; IPR00071
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PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA : : | : | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | | : | : | | | : | : | | | | : | : | | : | | : | : | | | | : | : | : | | | | : | : | : | | | | : | : | : | | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                             RTEPSILNNYLIWNLVQKTTSSLDQRFETAQEKLLETLYGTKKSCTPRWQTCISNTDDAL
                                                                                                                                                                                         IYHKMSISELQALAPAVDWLEFLSFLLSP---
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                                                                                                                                                                                                                                                                                            -NRTANEKVLTAYLDYMVELGVLLGGQPTSTREQMQQVLELEIQLANITVPQDQRRDEEK
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267; Conserv
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Last annotation update)
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Pred. No. 3.1e-75;
4; Mismatches 312;
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Search completed: May 21, 2003, 18:49:07 Job time: 46 secs

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
3952
3928
1375.5
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1351
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3958
1 MEAETGSSVETGKKANRGTR......AFNCPPNSTMNRGMDSCRLW 749
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1: /SIDS2/gcgdata/s
2: /SIDS2/gcgdata/a
                                                                                                                                                                                                                                                Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*
| A_Geneseq_101002:*
| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1982.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1982.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1983.DAT:*
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Human PKO POTYPEPC Polypeptide homolo Amino acid sequenc Drosophila melanog	AAU29233 AAB67845 AAU82722 ABB61898	222	736 883 766 661	30.8 30.6 30.5	1223 1221 1221 1212 1205.5
Human PRO403 prote		20	736 736		1223
	AAR76236	16	708 754		1241.5
Bowine endocheiin		19	758	31.5	1248.5
M		23	753	31.7	1256
		17	758 758	31.8	1257
Human endothelin		23	753	31.8	1257
		16	753	31.8	1257
the telephone communication of		16	753	31.8	1257
Human pracentar en		16	703	31.8	1257
Rat enkepharinase		15	750	31.9	1263.5
Enkephalinase (rat		9	750	31.9	1263.5
Atrial natriuretic	AAP82940	۽ م	750	33.1	7/71
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Ď.	AAPYOSYS	5	750	32.2	1275.5
Human common acute	AAR5270	5 5	748	32.4	ω
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TOPE OF COURT		23	779	33.7	1332.5
•	ABB7	23	779	33.7	ယ္သ

## ALIGNMENTS

AAY96190;

(first entry)

Human PHEX. 19-DEC-2000 AAY96190 standard; protein; 749 AA.

PHEX; human; metalloprotease; endopeptidase; X chromosome; X-linked hypophosphatemia; hyperphosphatemia; hyperparathyroidism; renal osteodystrophy; phosphaturia; therapy; diagnosis. Homo sapiens. 31-AUG-2000. WO200050580-A2. Peptide WPI; 2000-565455/52 Crine P, Boileau G; 24-FEB-1999; (UYMO-) UNIV MONTREAL. 24-FEB-2000; 2000WO-CA00201. 99CA-2262056 Location/Qualifiers /label= Transmembrane\_domain

A human neutral

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The present sequence is that of human PHEX (a gene product of phosphate-regulating gene with homology to endopeptidase on X chromosome). Absence of a functioning PHEX gene is associated with 2C chromosome). Absence of a functioning PHEX gene is associated with 2C myophosphatemia. PHEX is a type II integral membrane glycoprotein. 2C was modified with a signal peptidase coding sequence (see ANY96188 CC and ANY96189). The soluble PHEX thus comprised the active ectodomain. 2C constructed by replacement of the 2C waline. Soluble and inactive mutant forms of PHEX can be used to creen ligands to PHEX. These ligands are used as substrates are used to treat phosphaturia and/or hypophosphatemia. A constructed for phosphaturia, an inhibitor 2C substrate for PHEX, or PHEX itself, can be used to treat phosphaturia and/or hypophosphatemia. A 2C hyperphosphatemia, including its most frequent manifestations, according to the constructions.
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601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
                        601 PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
                                                                                         541 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD
                                                                                                                                                                                      481 FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF
                                                                                                                                                                                                                                  481 FIMNDTHVNEDLKAIKESEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
                                                                                                                                                                                                                                                                             421 MFYDYYFQEDKKEMMEELVEGYRWAFIDMLEKENEWMDAGTKRKAKEKARAYLAKYGYPE 480
                                                                                                                                                                                                                                                                                                                       421 MFVDVYFQEDKKEMMEELYEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 64pp; English.
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The present sequence is encoded by the human PEX gene. The PEX gene spans the deleted region xp22.1 in x-linked hypophosphatemic rickets. The gene is mutated in non-deletion patients with the disorder. PEX is a cell membrane-associated protein with its active site in the extracellular compartment. The cells with the highest level of PEX expression are the

Disclosure; Fig 2A; 52pp; English

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AAY84627
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                                                                                 Diagnosis and treatment of metabolic bone diseases e.g. osteomalacia and osteoporosis comprises determining the level of parathyroid hormone
                                                                               related peptide in a patient -
                                                                                                                             N-PSDB; AAA12670.
                                                                                                                                                           Karaplis AC, Goltzman D,
                                                                                                                                                                                                       28-SEP-1998;
                                                                                                                                                                                 (UYMC-) UNIV MCGILL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PEX gene; xp22.1; x-linked hypophosphatemic rickets; osteoblast; parathyroid hormone; PTH; osteoclast; bone; bone breakdown; parathyroid hormone related peptide; PTHrP; metabolic bone disease; osteomalacia; osteoporosis; osteopetrosis; Paget's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748;
                                                                                                                                                                                                                                                                    FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF
                                                                                                                                                                                                                                                                                                                                     TIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALFYVVGK 420
                                                                                                                                                                                                                                                                                                     FIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAF 540
                                                                                                                                                                                                                                                                                                                                                                      MFYDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE 480
                                                                                                                                                                                                 YSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLD 600
                                                                                                                                PWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKW 660
ISNFEEFQKAFNCPPNSTMNRGMDSCRLW 749
                              ISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                 INDRROGLEEPLLPGITFINNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA
                                                                                              INDRROGLEEPLLPGITFINNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oncogenous hypophosphataemia osteomalacia; chronic renal failure; idiopathic hypercalcuria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant tumour PEX protein; phosphate regulating gene; inhibition; endopeptidases; metalloendopeptidase; tumour; OHO; PEX active site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9810078-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-1997;
                                                                                                                                                                                                                                                                                                                                protein a product of a phosphate regulating gene with homology to endopeptidases, suggesting that PEX might be a metalloendopeptidase. It was isolated from tumours causing oncogenous hypophosphataemia osteomalacia (OHO). Compounds which are targeted to inhibit PEX active site, identified in the method of the invention, are useful for the treatment of hyperphosphataemia or chronic renal failure. PEX can also be used as a target for the treatment of idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the recombinant human tumour PEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human PEX - useful for the treatment of hyper:phosphataemia or chronic renal failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV23264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goltzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1A-1G; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KARA/)
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                       hypercalcuria.
                                        181 SERKESLLQTLATERGQYSNSVETRLYVSSDDKASNEHILKLDQATLSLAVREDYLDNST 240
                                                                                                      121 KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
                                                                                                                               61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                                                                                                                61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                                                                                                                                                                   1 MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
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                                                                                                                                                                                                                                                        Joca L
                                                                                                                                                                                     MEAETGSSVETGKKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECI 60
                           KSISRRRDTEAIQKAKILYSSCMNEKAIEKADGKPLLHILRHSPFRWPYLESNIGPEGVW
EAKSYRDALYKEMYDTAVLLGANSSRAEHDMKSYLRLEIKIAEIMIPHENRTSEAMYNKM 300
                                                                                                                                                                                                                                           745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOLTZMAN D.
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                                                                                                                                                                                                                                                       Similarity
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Pred. No. 0;
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Claim 2; Fig 3; 59pp; English.
                      Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                         N-PSDB; AAA63763.
                                                                                                                             Desgroseillers L, Boileau G;
                                                                                                                                                             (UYMO-) UNIV MONTREAL.
                                                                                                                                                                                         11-FEB-1999;
                                                                                                                                                                                                                 11-FEB-2000; 2000WO-CA00147.
                                                                                                                                                                                                                                                 17-AUG-2000
                                                                                                                                                                                                                                                                            WO200047750-A2.
                                                                                                                                                                                                                                                                                                                    NEP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism.
                                                                                                                                                                                                                                                                                                                                                                                         A murine neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                                                                                                                                                                                                                                              Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08130;
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Retallopeptidase-like enzyme, designated NL-1. The specification

also describes NL-2 and NL-3. The NL enzymes are used to test for

specific inhibitors. The N-terminal region of the enzymes can be used

to promote production and secretion of foreign proteins and active

chimperides, using chimeric constructs containing the foreign protein

chimperides, using chimeric constructs and may be useful in the

chimperides and in phase with the N-terminal region. The NL enzymes

chimperides and may be useful to disease, pain,

chimperides, and may be used to control fertility. They have

chimperides and ovaries, and may be used to treat bone diseases,

chimperides, and may be used to treat bone diseases,

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710 HSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                     670 VRQAYKAYLRWLAD---GGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
                                                                                                                    650 LREAFRAYRKWINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGA 709
                                                                                                                                                                                                                                           591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 491 REQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 LAKVGYPEFIM--NDTHVNEDLKAIKESEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 NMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN-WMDEESKKKAQEKANNI 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 ILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIES 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 HRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELF-----PDEEVVVYGIPYLENLED 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 NKMNISELSAM--IPQFDWLGYIKKV---IDTRLYPHLKDISPSENVVVRVPQYFKDLFR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 VRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALY 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 YRDALYKFMYDTAYL-----LGANSSRAEHDMKSYLRLEIKIAEIMIPHENRTS-EAMY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 --PAVEKÄKTLYRSCMNQSVIEKRDSEPLLSVLK-MVGGWPVAMDK-----WNETMGLK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 SKVNLSVDPCDNFFRPACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GAIVTLGVFYSIGKOLPLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARIL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GTRIALVVF--VGGTLVLGTILF-----LVSQGLLSLQAKQEVCLKPECIEAAAAIL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                  RNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGG
                                                                                                                                                                                                                                                                                                          IIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKDQPQSLNFGGIGMVIGHEITHGFDDNG
                                                                                                                                                                                                                                                                                                                                                                     ETNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WELERQLAVINSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHK- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%; Score 1375.5;
38.8%; Pred. No. 4.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The NL enzymes
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727 HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMKRCRIW 765

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RESULT 5
                                                                                                         SNEPD or SNEPD control the proteins may all yearning control to state country of the state country of the state and care and genomic clones of SNEP homologues; cas research reagents and material for the discovery of treatments and disgnostics for animal and human diseases; and for chromosome country country of the state of identification. The SNEP proteins may be used as immunogens to compose the country chromatography. SNEP proteins may also be used in screening for compounds which modulate country country, and to assess enzymatic cleavage of small conclude substrates in cells, cell-free preparations, chemical libraries cand product mixtures. The SNEP proteins (as vaccine compositions), country chromatography. CC SNEP nucleotides, and SNEP activators or inhibitors may used concluded and chronic renal insufficiency, renal and hepatic country is careful to treat acute and chronic renal insufficiency, renal and hepatic country is careful to the careful and chronic renal insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice variant; alternative splicing; zinc endopeptidase family; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neuronal disease; panoreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neprilysin-like membrane metallopeptidase SNEPb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and pertide hormones. SNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 33-35; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and hepatic ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jagerschmidt A,
well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases. they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNBPa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-212582/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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AAB83842 ID AAB

AAB83842 standard; Protein;

753 AA

RESULT

AAB83842; 23-JUL-2001

(first entry)

Amino acid sequence of a human metalloprotease enzyme IGS5.

anorexia; bulimia; asthma; Parkinson's

disease;

diabetes; obesity; acute heart failure;

Metalloprotease; IGS5; infection; pain; cancer;

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                                                                                                                                                                                                                                                                                                                        475
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                                                                                                                                                                                                                                      535 PNLWIIGAAVVNAFYSPNRNQIVFPAGILOPPFF-SKEQPQALNFGGIGMVIGHEITHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRYSIFDVLRDELEVILKAVLEN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VESAGRAGQKRPGFLEGGLLLLLLLVTAALVALGVLYADRRGIPEAQEVSEVCTTPGCVI 70
                                                                            654
                                                                                                                                                                                                587
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711 KTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKERCRVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMVQVLELETQLAKATVPQEERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STA---KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-EVVGGWPVAMDR------WN
                                                                                                                                                                                                                                                                                                                                                                                                YVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVETLD-ELGWMDEESKKKAQEK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                        FIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVNYRKALFGTMVEEVRWRECVG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVIALYHRMGLEELQSQFGLKGFDWTLFIQTVLSS-----VKIKLLPDEEVVVYGIPYLQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSENVVVRVPQYFK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMKSVLRLEIKIAEIMIPHENRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDN 238
                                                                                                                                                                                           DNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAG-LNVKGKRTLGENIA 645
                                                                                                                                                                                                                                                                            KTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGF
                                                                                                                                                                                                                                                                                                                    AMSIREQIGHPDYILEETNRRLDEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVD 534
                                                                                                                                                                                                                                                                                                                                                          ARAVLAKVGYPEFIMNDTH---VNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVP 526
                                 QIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                               DNGGLREAFRAYRKWINDRRQGLEEPLLPGITFINNQLFFLSYAHVRCNSYRPEAAREQV 705
                                                                                                                                                          DINGRNITAKINGNMANDWWSNIFSTQHFREQSECMIYQYGNYSWDLADEQNVNGFNTLGENIA
                                                                            DNGGVRQAYKAYLKWM----AEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFÅIQSI
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38.6%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1362; DB 22; Pred. No. 6.6e-108;
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CC IGSS IGSS polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, CC urinary retention, osteoporosis, anglina pectoris, myocardial infarction, CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, CC psychotic and neurological disorders, autism, multiple sclerosis, cpsychotic and neurological disorders, autism, multiple sclerosis, CC Alzheimer's disease, and other neurodegenerative diseases, sleep CC disorder, epilepsy, cardiovascular disease, arteriosclerosis, cerebral cc infarction, peripheral vascular disease, Raynaud's disease, kidney CC diseases, gastric emptying, post-operative or diabetic gastroparesis, cof delayed gastric emptying, post-operative or diabetic gastroparesis, clambure disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such a unnetimental adaptation and dyskinesias, such
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                  as Huntington's disease or Gilles de la Tourette's syndrome.
122 SISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human metalloprotease enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 9-10; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1999; 99EP-0203862.
19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzhehner's disease; neurological disorder; autism; multiple sclerosis; Alzhehner's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm; subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deleersnijder W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SOLV ) SOLVAY PHARM BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136610-A1.
                                         71 AAARILONMOPTTEPCDDFYQFACGGWLRRHVIPETNSRYSIFDVLRDELEVILKAVLEN 130
                                                                                62 AAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                              11 VESAGRAGQKRPGFLEGGLLLLLLLVTAALVALGVLYADRRGIPEAQEVSEVCTTPGCVI 70
                                                                                                                                                                       9 VETGKKANR-----GTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIE 61
                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                               293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-343815/36
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF89739.
                                                                                                                                                                                                                                                                                                                    753 AA;
                                                                                                                                                                                                                          Conservative 153; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiegers
                                                                                                                                                                                                                                               34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹,
                                                                                                                                                                                                                                               Score 1352; DB 22;
Pred. No. 4.8e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weske M;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                               Length 753;
                                                                                                                                                                                                                   44; Gaps
                                                                                                                                                                                                                   18;
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Ş 밁 Ş В Š

Schwartz JC;

Gros C,

Haret C,

Bonhomme MC,

Facchinetti P;

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RESULT 7
AAY44177
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             Ouimet T,
                                                                                 08-APR-1998;
                                                                                                                                                                                                                                                                                    Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder;
                                            (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                     08-APR-1998;
                                                                                                                                                      15-OCT-1999
                                                                                                                                                                                       FR2777291-A1
                                                                                                                                                                                                                                                                    cardiovascular disease; neurodegenerative disease; growth
                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2000 (first entry)
                                                                                                                                                                                                                         Rattus rattus
                                                                                                                                                                                                                                                       hypothalamic-hypophyseal axis; endocrine disorder
                                                                                                                                                                                                                                                                                                                                            Rat membrane metalloprotease NEPII protein.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44177 standard; Protein; 774 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    706 QIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 YVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVETLD-ELGWMDEESKKKAQEK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 ARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 DLFRILGSERKKTIANYLVWRMYYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 FIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 DVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS-----VKIKLLPDEEVVVYGIPYLQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 ER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 SE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSENVVVRVPQYFK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMMQVLELETQLAKATVPQEERH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 STA--KDRPAVEKARTLYRSCHNQSVIEKRGSQPLLDIL-EVVGGWPVAMDR-----WN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKERCRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQV 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVNGFNTLGENIA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNNGRKYDKNGNLDPWWSTESBEKFKEKTKCMINQYSNYYWKKAG-LNVKGKRTLGENIA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQPQALNFGGIGMVIGHEITHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGF 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLENIIDTYSARTIQNYLYWRLYLDRIGSLSQRFKDTRVNYRKALFGTMVEEVRWRECVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMKSVLRLEIKIAEIMIPHENRT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98FR-0004389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin, disturbances of the hypothalamic-hypophyseal axis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the rat membrane metalloprotease designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 12-16; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potentially useful for treating e.g. cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ28810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 VREAYLQFMTSVATMLRRDLNLPGETDLVQEEMAQVLHLETHLANATVPQEKRHDVTALY 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                       384 VFPAQTLQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTMEEVRWRECVSYVNSNME 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 NKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                              444 SAVGSLYIKRAFSKDSKSIVSELIEKIRSVFVDNLDELN-WMDEESKKKAQEKALNIREQ
                                                                                                                                                                                                                                                                      476 VGYPEFIM--NDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POCCET
                                                                                                                                                   563 AAVVNAFYSPNRNLIVFPAGILQPPFF-SKDQPQALNFGGIGMVIGHEITHGFDDNGRNF 621
                                                                                                                                                                                         534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrine disorders.
682 AYKAYLQWL---AEGGRDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAIQSIKTDVHSP
                                   653 AFRAYRKWINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-593429/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAIVTLGVFYSIGKOLPLLNSLLHVSRHERTVVKRVLRDSSQKSDICTTPSCVIAAARIL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTRIALVVF--VGGTL-VLGTILF-----LVSQGLLSLQAKQEYCLKPECIEAAAAIL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKYNLSYDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER---K 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRDALYKFMVDTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNMDQSKKPCDNFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSSVQHR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PAVEKAKTLYRSCHNQSVIEKRDSEPLLNVL-DMIGGWPVAMDK-----WNETMGPK 209
                                                                                                                                                                                                                                                                                                                                                                                                                            SERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRMGLEELQERFGLKGFNWTLFIQNVLSSVQV----ELLPNEEVVVYGIPYLENLEEIID 383
                                                                                                                                                                                                                                                                                                                                                 YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289;
                                                                           DKNGNMLDWWSNFSARHFRQQSQCMIYQYSNFSWELADNQNYNGFSTLGENIADNGGVRQ
                                                                                                              DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE 652
                                                                                                                                                                                                                                 IGYPDYILEDNNRHLDEEYSSLTFSEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 156; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1351; DB 20;
pred. No. 6.1e-107;
6; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AAB60561
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AX

The invention relates to the human SNEPA, SNEPB and SNEPC proteins, and the cDNAs encoding them. SNEPA, SNEPB and SNEPC are neprilysin-like considered the control of the substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the conclectides may be used as hybridisation probes for cDNA and genomic consists of isolate full-length oDNAs and genomic clones encoding SNEPA.

CC DNA; to isolate full-length oDNAs and genomic clones encoding SNEPA.

CC SNEPB or SNEPC; to isolate cDNA and genomic clones of SNEP homologues; SNEPB or SNEPC; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and conditional control of the discovery of treatments and continuation. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPA, SNEPB or SNEPC. Such control of the discovery of treatments and control of the discovery of treatments and control of the snew proteins may be used as immunogens to produce antibodies immunospecific for SNEPA, SNEPB or SNEPC. Such considered the proteins of the snew proteins of the sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neuronal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory; cerebroprotective; hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neprilysin-like membrane metallopeptidase SNEPa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB60561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB60561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; SNEPa; neprilysin-like membrane metallopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1069188-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute chronic renal insufficiency, pain, stroke, cancer, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 28-30; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jagerschmidt A, Agnel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and hepatic ischemia
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     23-JUL-2001 (first entry)
                                               AAB83841;
                                                                            AAB83841 standard; Protein; 779
                                                                                                                                                                             776 CRVW 779
                                                                                                                                                                                                                 746 CRLW 749
                                                                                                                                                                                                                                    717 INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER 775
                                                                                                                                                                                                                                                                        686 LSYAHVRCNSYRPEAAREQYQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
                                                                                                                                                                                                                                                                                                               660 WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF
                                                                                                                                                                                                                                                                                                                                                 627 WKKAG-LNVKGKRTIGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFINNQLFF 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEETNRRLDEEYSNLNFSEDLYFENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 YRKALFGTMVEEVRWRECVGYYNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMYYSRIPNLSRRFQYRWLE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory or hepatic diseases, they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFDWTLFIQTVLSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 SYLRLEIKIABIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLL--GANSSR----AEHDMK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 EVVGGWPVAMDR-----WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GYYPWLRHNYDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 QGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                      QALNEGGIGMVIGHEITHGEDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS
                                                                                                                                                                                                                                                                                                                                                                                                              RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQNLKYGAQRSLRKLREKYDDNLWIIGAAVVNAFYSPNRNQIVFPAGILQDPFF-SKEQP 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQTRKYLAQSDEFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKNFVDVYFQEDKKENMEELVEGVRWAFID 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      779 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 144; Mismatches 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.9%; Score 1343.5; DB; 39.5%; Pred. No. 2.7e-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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Qy Db

102 GYYPWLRHNYDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161

77 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 136

42 QGLLSLQAKQEYCLKPEGIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101

Query Match Best Local ( Matches 28

Local Similarity

284; Conservative

33.7%; Score 1333.5; DB 39.2%; Pred. No. 2e-105; tive 145; Mismatches 25

DB 22; Length 779; 05; 258; Indels 37;

37; Gaps

17;

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Sequence
                                diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of
                                                                                                                                                                                                cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions
                                                                                                                                                                                                                                                                                                        Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                        urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, management of the part of the p
                                                                                                                                                                                                                                                                                                                                                                                   psychotic and neurological disorders, autism, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human metalloprotease enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 8; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF89738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deleersnijder W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm; subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SOLV ) SOEVAY PHARM BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000; 2000WO-EP11532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulinia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human metalloprotease enzyme IGS5.
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779 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0203862
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AAB08131
ID AAB08
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                                                                                                                                                                                                                                                                 A human neutral endopeptidase metallopeptidase-like enzyme NL-2
                                                                                                                                                                                                                                                                                                  04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                AAB08131 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 HSPFRWPVLESNIGPEGVWSER----KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH
                 11-FEB-1999;
                                                11-FEB-2000; 2000WO-CA00147.
                                                                                 17-AUG-2000
                                                                                                                WO200047750-A2
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                             NEP-like enzyme; protein production; protein secuneurological disease; Alzheimer's disease; pain;
                                                                                                                                                                                                                              Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 TLD-ELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE
                                                                                                                                                                              fertility; bone disease; abnormal phosphate metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717
                                                                                                                                                                                                                                                                                                                                                                                                                                               776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVVGGWPVAMDR-----WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                               CRVW 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQNLKYGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDS 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER
               99CA-2260376
                                                                                                                                                                                                               secretion;
                                                                                                                                                                                                   psychiatric disorder,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human neutral endopeptidase metallopeptidase-like enzyme, designated NL-2. The specification also describes NL-1 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzyme are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                                                                          and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 4; 59pp; English.
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                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                         processing by the NL-3 enzyme.
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                                                                          128 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-
                                                                                                                                                                                                                                               Loca.
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EVVGGWPVAMDR-----WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH
                                                                                                                                                                                                                             284;
                                                                                                                                                                                                                                                 l Similarity
                                                                                                                                                                                                                                                                                                         770 AA;
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                                                                                                                                                                                                                                               33.7%; Score 1332.5; DB 2 39.2%; Pred. No. 2.4e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS-----
591 QALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 QGILSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSPFRWPVLESNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
                                                                                                                                                                                                                                                                                                                                FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
                                                                                                                                                                                                                                                                                                                                                                                 VKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
                                                                                                                                                                                          MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV 506
                                                                                                                                                                                                                                                                                   YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                   LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE
                                            RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKEKEKTKCMINQYSNYY 626
                                                                                           LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP
                                                                                                                                      LOTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYP 566
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                                                               especially male erectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention provides an assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and food intake disorders, such as obesity, bulimia, anorexia and
                                                                                                                                                                                                                  associated with male genitalia, in the preparation of a medicament for the treatment or prevention of male sexual dysfunction, especially male erectile dysfunction (MED). The NPY inhibitor
                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence of human SEP, a soluble secreted endopeptidase. The invention relates to the us of an inhibitor of NPY, or an inhibitor of NPY Y1 receptor, especially an inhibitor selective for an NPY or NPY Y1 receptor.
                                                            metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 9; 179pp; English.
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06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Naylor AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an inhibitor of neuropeptide {\bf Y} in the preparation of medicament e treatment or prevention of male erectile dysfunction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFIZER
                                                   disorders.
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2001GB-0011037.
2001US-0895367.
2001US-0905846.
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Neprilysin family; human; gene therapy; protein therapy; vaccine; neprilysin protease; pain; pain associated disorder; tissue injury; chest pain; complex regional pain syndrome; (RPS; headache; migrane; reflex sympathetic dystrophy; RSD; tooth pain; musculoskeletal disorder; joint pain; surgery; inflammation; irritable bowel syndrome; anaemia; aberrant spermatid cell activity; infertility; cancer; brain disorder;
                                                                                                                                  Novel neprilysin family protein, 56638.
                                                                                                                                                                        18-JUN-2002
                                                                                                                                                                                                                                          AAU78850 standard; Protein; 779
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The invention describes nucleic acids (I) encoding a novel human Maprilysin protease (II). (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate neprilysin protease expression e.g. by rectifying mutations or deletions in a patient's genome that affect the activity of the protease by expressing inactive proteins or to supplement the patients own production of the protease. (I) And its complementary sequences may also be used as similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) and (II) may be useful in the treatment of pain or pain associated disorders including tissue injury, chest pain, recomplex regional pain syndrome (CRPS), reflex sympathetic dystrophy and the protease of the protein associated disorders are accomplexed.
                               (RSD), tooth pain; headaches e.g. migrane, and pain associated with musculoskeletal disorders e.g. joint pain, surgery and inflammation e.g. irritable bowel syndrome. (II) may also be useful in the treatment of disorders including anaemia, infertility, aberrant spermatid cell activity, cell proliferation and/or differentiative disorders e.g. cancer and brain disorders e.g. cerebral edema, neurodegenerative diseases e.g. Alzheimer's disease, cerebrovascular disease, haematopoietic neoplastic disorders, immune disorders and erythroid associated disorders e.g. erythroblastosis. This is the amino acid sequence of the novel human
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immune disorders and erythroid stosis. This is the amino acid a family protein 566368.
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Query Match 33.7%; Score 1332.5; DB 23; Length 779; Best Local Similarity 39.2%; Pred. No. 2.4e-105; Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;
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Phillips

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                                                                                                                                          enzyme; gynaecological; antisense-therapy; male erectile dysfunction
MED; female sexual dysfunction; FSD; female sexual arousal disorder;
    Domain
                                                                      Homo sapiens
                                                                                                                                                                                          Human; secreted
                                                                                                                                                                                                                                      Human soluble secreted endopeptidase (SEP) protein.
                                                                                                                                                                                                                                                                                      07-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LK-DISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIYIDQPTLGMPSREYYFNGGSNRK.-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVVGGWPVAMDR----
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                                                                                                                    premature
                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  779
                                                                                                                                                                                                                                                                                    (first entry)
  Location/Qualifiers 570..779
                                                                                                                    ejaculation;
                                                                                                                                                                                          endopeptidase; SEP; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH
                                                                                                                    anorgasmia; vaginismus
                                                                                                                                                                                          vasotropic;
                                                                                                                                                                  dysfunction;
                                                                                                                                                                                          analgesic;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD) (e.g. female sexual arousal disorder (FSD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is human SEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 162; 167pp; English.
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                                                                      FSRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFID 448
                                                                                                                                            QVLELETQLAKATVPQEERHDVIALYHRMGLEELQSQFGLKGFNWTLFIQTVLSS-----
                                                                                                                                                                                                                                                              SVLRLEIKIAEIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGIPEAQEVSEVCTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPETNSRY
                             YRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVE
                                                                                                                                                                                                                                                                                                            IIYIDQPTLGMPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMV
                                                                                                                                                                                                                                                                                                                                                        ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
                                                                                                                                                                                                                                                                                                                                                                                                      EVVGGWPVAMDR-----WNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIFDVLRDELEVILKAVLENSTA - - KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-
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                                                                                                                      VKIKLLPDEEVVYYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                               HSPFRWPVLESNIGPEGVWSER----KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284;
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Pred. No. 2.4e-105;
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RESULT 14
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ID AABB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; parkinson's disease; acute heart failure; hypotension; hypotension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease; neurological disorder; autism; multiple sclerosis; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a His-tagged metalloprotease enzyme IGS5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFF 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFF-SKEQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de la Tourette's syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 79
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561
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453
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273
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                                                                                                                                                                                  note= "N-glycosylation site"
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355 EEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVRTVFVETLD-ELGWMD

LLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMD

VVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTT 398

VVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDTRVNYRKALFGTMV 354

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19-NOV-1999;
31-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, psychotic and neurological disorders, autism, multiple sclerosis, alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovascospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular diseases, Raynaud's disease, kidney diseases, gastrointestinal disorders, mottlity disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyakinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a His-tagged metalloprotease designated IGS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, etrobe inforce allowatch beautiful procession and pectoris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000; 2000WO-EP11532
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                                                                                          181
                                                                                                                                  229 LAVREDYLDNSTEAKSYRDALYKFMYDTAVLL--GANSSR----AEHDMKSVLRLEIKIA 282
                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                112 DLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                             52 EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNV 111
                                          EIMIPHENRTSE-AMYNKMNISELSAM--IPQFDWLGYIKKVIDTRLYPHLK-DISPSEN 338
                                                                                     MPSREYYFNGGSNRK-VREAYLQFMVSVATLLREDANLPRDSCLVQEDMMQVLELETQLA 239
                                                                                                                                                                                DR-----WNETYGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQFTLG 180
                                                                                                                                                                                                                        SNIGPEGVWSER---KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLS 228
                                                                                                                                                                                                                                                                        EVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL-EVVGGWPVAM 126
KATVPQEERHDVIALIHRWGLEELQSQFGLKGFNWTLFIQTVLSS-----VKIKLLPDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       702 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 143; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-0203862.
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RESULT 15
AAB83840
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KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW henign prostatic hypertrophy; migraine; psychotic disorder; allergy;
KW benign prostatic hypertrophy; migraine; psychotic disorder; disease;
KW cardiovascular disease; sleep disorder; pellepsy; kidney disease;
KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW peripheral vascular disease; Raynaud's disease, motility disorder;
KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW dastrointestinal disorder; astric emptying; gastroparesis; diarrhoea;
KW inflammation; chemotherapy induced injury; tumour invasion;
KW inmune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW severe mental retardation; dyskinesia; Huntington's disease;
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19-NOV-1999;
31-MAY-2000;
          Claim 3; Page 6; 115pp; English
                                                             New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
                                              diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                            Deleersnijder W, Wiegers R,
                                                                                                                                       N-PSDB; AAF89737
                                                                                                                                                          WPI; 2001-343815/36.
                                                                                                                                                                                                                                    (SOLV ) SOLVAY PHARM BV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFNTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFFINYAQVWCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTKRKAKEKARAVLAKVGYPEFIMNDTH--VNEDLKAIKFSEADYFGNVLQTRKYLAQS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGV 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de la Tourette's syndrome.
                                                                                                                                                                                                                                                                        ; 99EP-0203862.
; 99NL-1013616.
; 2000EP-0201937.
; 2000NL-1015356.
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641 PEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPMH-PKERCRVW
                                          698 PEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                        584 NTLGENIADNGGVRQAYKAYLKWM---AEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYR
                                                                                                                                        638 RTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYR 697
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Sequence 25, Appl
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INFORMATION FOR SEQ ID NO:
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                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                     SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt, APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz. TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
                                                                                                                                                                             COMPUTER: IBM AT-compatible, 80486 OPERATING SYSTEM: MS-DOS version 6
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
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                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPDL----YFENAMRF-----FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYS
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                                                                                                                                                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                      D.C
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                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                   Diskette, 3.5 inch, 1.4 Mb storage
                       11-NOV-1994
                                          PCT/EP94/03706
                                                                                                                      US/08/646,273
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US-08-289-112-2

Sequence 2, Application US/08289112 Patent No. 5688640

GENERAL INFORMATION: APPLICANT: Yanagi

APPLICANT: Yanagisawa, Masashi TITLE OF INVENTION: Endothelin Converting Enzyme-1: A TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1

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                                                                   670 -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS
                                                                                                                                                613 WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
                                                                                                                                                                                   603 WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
                                                                                                                                                                                                                            554 PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW
                                                                                                                                                                                                                                                               543 ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                      438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNF 80
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                                                                                                      DRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
NSKEFSEHFRCPPGSPMN-PPHKCEVW 753
                                     NSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                             NEDLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE
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NUMBER OF SEQUENCES:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:414/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 10-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       381
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TELEFAX: 79-0924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
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ZIP: 77210-4433
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                                                                                                                                                                                                                                         -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYRAC 173
                                 DLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSAS 544
                                                                                                                  EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM-----NDTHVNE 490
                                                                                                                                                                                                   RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV 439
                                                                                                                                                                                                                                                                               VIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSR 380
                                                                                                                                                                                                                                                                                                                          GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF---
                                                                                                                                                                                                                                                                                                                                                            NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
                                                                                                                                                                                                                                                                                                                                                                                                      FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                              FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNETRIEELKAKPLMELIEKLG-GWNI----TGPWDKDNFQ--DTLQVVTSHYHTSP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
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                                                                            LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 515
                                                                                                                                                          RFQDADEKFMEYMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII 456
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P.O. Box 4433
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----YFENAMRF-----FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT 560
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US-08-646-273-23
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-NOV-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage COMPUTER: IBM AT compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.0 SOFTWARE: WordPerfect version 5.1
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                                                                                                                                                                66 YACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC 123
                                                                                                                                                                                                         83 FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSC 142
                                                                                                                                                                                                                                                                                          23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 11-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                 7 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 65
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FFSYYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG
                          FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLLGA 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNEIVFPAGILQAPFYTRSS-PNALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPWWK 619
                                                                                MNETRIEELKAKPLMELIEKLG-GWNI-
                                                                                                                       MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
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                                                                                                  FILING DATE: 11-NOV-1 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: Wordberfect version 5.1
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 754 amino acid
                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt, APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                           FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                           TOPOLOGY:
                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                              APPLICATION NUMBER: PCT/EP94/03706
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US-08-574-763-2
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                                                                                                                                                        GENERAL INFORMATION:
                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                              APPLICANT:
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                                       STREET: P. O. CITY: Houston
COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                            STATE:
                                                                    ADDRESSEE:
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                                                         O. Box 4433
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sequence 2, Application US/08574763 Patent No. 5736376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   725 EEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 GAEDTIRPOMOQILDFETALANITIPOEKRRDEELIYHKVTAAELOTLAPAINWLPF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 YACGGWIKANPYPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSSVEAFKQQTACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--K
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                                                                                                                                                     Yanagisawa, Masashi
Arnold, White &
                                                                                                   ENZYME-2 AND
                                                                                                                             RECOMBINANT ENDOTHELIN CONVERTING
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                                                                                                   ITS USE
                                                                                                   IN ECE INHIBITOR SCREENING
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 GPWDQDNF--MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 NT-TFNSSSEAERKTORFYLSCLOVERIEELGA----HALRD------LIDKIGGWNVT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KSISRRRDTEAIOKAKILYSSCMNEKAIEKADAKPLLHILRHSPERWPVLESNIG---PE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 RVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNNSNSLWDQNQAILKHLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: Co
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                402
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                                                                                                                                                                                                                           521 IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ 580
                                                                                                                                                                                                                                                                          476
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                                                                                                                                                                                                                                                                                                                    462 FALGSLFVKATFDRQSKETAEGMISETRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQYHRDPSHSTCLTEACI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
656 AYRKWINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715
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                                                                                                                                                                                                                                                                                                                                                            YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRTANEKVLTAYLDYMEELGMLLGGQPTSTREQMRQVLELEIQLANITVPQDQRRDEEKI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSTEAKSYRDALYKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAM 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHKMSTAELQALAPSMDWLEFLSFLLSP-----LELGDSEPVVVYGTDYLQQVSELINR 401
                                                                                                                                   TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK 639
                                               EGNLRÞWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 697
                                                                                         NGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFR 655
                                                                                                                                                                              TVNAFYSASTNQIRFPAGELOKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595
                                                                                                                                                                                                                                                                       VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
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APPLICANT: SmithKline Beecham plc
TITLE OF INVENTION: No. 6255488el
FILE REFERENCE: GP30124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/305,640B CURRENT FILING DATE: 1999-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             698 AYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARF 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716 RVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
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632 LHWWTEASYSRFLRKAECIVRLYDNFTVYNQR----VNGKHTLGENIADMGGLKLAYHAY 687
                                                                                                                  540 FYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNL 599
                                                                                                                                                                                                                                                                       455 ALFVHEHFSAASKAKVQQLVEDIKYILGQRLE-ELDWMDAETRAAARAKLQYMMVMVGYP
                                                                                                                                                                                                                                                                                                                    420 KMFYDYYFQEDKKEMMEELVEGYRWAFIDMLEKENEWMDAGTKRKAKEKARAYLAKYGYP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 LVVFVGGTLVLGTILFLVSQGLLSL--QAKQEYCLKPECIEAAAAIL-SKVNLSVDPCDN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 24.8%; Score 983.5; DB 4; Length 775; Local Similarity 31.0%; Pred. No. 6.8e-88; ses 233; Conservative 158; Mismatches 294; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVLGTLSNSRDFLRHFGCPVGSPMNSG-QLCEVW 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KITPHLRWKWLLDQIFQ------EDFSEEEEVVLLATDYMQQVSQLIRSTPHRVLHNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVFMERVLSLLGADA--VEQKAQEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKEMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHEN---RTSEAMYNKMNISELS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLYKAQGVYSAAALFSLTVSLDDRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSCLDMREIERLGPRPMLEVIEDC-------GGWDLGGAEERPGVAARWDLNR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW-----SER-----KFSLLQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILY 139
                                                                                                                                                                                                                                                                                                                                                                  VWRVVVVLSEHLSPPFREALHELAQEMEGS-----DKPQELARVCLGQANRHFGMALG
                                           DPWWSTESEEKFKEKTKCMINQYSNY--YWKKAGLNVKGKRTLGENIADNGGLREAFRAY 657
                                                                                                                                                                                                                                                                                                                                                                                                             VWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDK-----CVNFIESALPYVVG 419
                                                                                        YYLPNKNOMVEPAGILO-PTLYDPDEPOSLNYGGIGTIIGHELTHGYDDWGGQYDRSGNL 631
                                                                                                                                                                                                                            EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNA 539
                                                                                                                                                                                   DFLLKPDAVDKEYE-FEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLLPPQALNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/EP FILING DATE: 11-NOV-1994 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PCT/EP94/03706
291 WKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEIILEIKKAFEESL-STLKWMDEDTR 349
                                       403 WDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTK 462
                                                                                     231 KEYLSKYSTLINSTDKCLLNNYMIWNLYRKTSSFLDQRFQDADEKFMEVMYGTKKTCLPR 290
                                                                                                                              344 PQYFKDLFRILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQ 402
                                                                                                                                                                          177 TIPQEKRRDEELIYHKYTAAELQTLAPAINWLPF----LNTIFYP--VEINESEPIVIYD 230
                                                                                                                                                                                                                                                               118 GLGLPSRDYYL-NKTENEKYLTGYLNYMYQLGKLLGGGAEDTIRPQMQQILDFETALANI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt, APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
                                                                                                                                                                                                                   285 MIPHENRTSEAM-YNKMNISELSAMIPQEDWLGYIKKVIDTRLYPHLKDISPSENVVVRV 343
                                                                                                                                                                                                                                                                                                                                                                                             166 RWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQA 225
                                                                                                                                                                                                                                                                                                        226 TLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLLGANS-SRAEHDMKSVLRLEIKIAEI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 WIRHNVDLKIKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLIHILRHSPF 165
                                                                                                                                                                                                                                                                                                                                                    67 GWNI-----TGPWDKDNFQ--DTLQVVTSHYHTSPFFSVYVSADSKNSNSNVIQVDQS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                       12 W-EHNQAI-IKHLLENSTA--SYSEAERKDQEYYRACMNETRIEELKAKPLMELIEKLG- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 LGSVSQFEEFGRAFHCPKDSPMNPA-HKCSVW 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658 RKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRV 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage COMPUTER: IBM AT-compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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CITY: Washington
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US-08-646-273-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08646273 Patent No. 6066502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage COMPUTER: IBM AT-compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.0 SOFTWARE: Wordberfect version 5.1 CURRENT APPLICATION NUMBER: US/08/646,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
176 PGSPMN-PHHKCEVW 189
                                                                    116 TLGLTNNQLFFLSFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSISNSKEFSEHFHCP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                      735 PNSTMNRGMDSCRLW 749
                                                                                                         675 GITFTUNOLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCP 734
                                                                                                                                                                           615 TKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLP 674
                                                                                                                                                                                                                                                                          555 LOKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEK 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt, APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
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                                                                                                                                                    61 TACMVEQYGNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ-TLP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV--KKNGAEQ-TLPTLGLINNQLFFL 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 KKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLDGITFTNNQLFFL 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 SLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYW 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 --FNFSWRYTADQLRKAPNRDQWSMTPPMVNAYYSPTKNEIVFPAGILQAPFYTRSS-PN 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 AQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 KSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVPDL-----YFENAMRF----
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                                                                                                                                                                                                                                   2 LQAPFYTRSS-PNALNFGGTGVVVGHELTHAFDDQGREYDKDGNLRPWWKNSSVEAFKQQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 amino acids
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-1994
                                                                                                                                                                                                                                                                                                                                      13.3%; Score 527.5; DB 3; Length 189; 51.8%; Pred. No. 6.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/EP94/03706
                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                   Gaps
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US-09-305-640-4

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GENERAL INFORMATION:

APPLICANT: SmithKine Beecham plc
TITLE OF INVENTION: No. 625546Bel Compounds
FILE REFERENCE: GP30124
CURRENT APPLICATION NUMBER: US/09/305,640B
CURRENT FILING DATE: 1999-05-05
UMMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Approximately No. 5834279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%; Score 246; DB 4; Length 181; Best Local Similarity 32.6%; Pred. No. 3.9e-16; Matches 62; Conservative 36; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE
LOCATION: (134)(145)(162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows SOTTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yang, Fude APPLICANT: Avarbock, David
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 GLKLAYHAIR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 TVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG---- 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 GLREAFRAYR 658
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                                                                                                                                                                                                                                                             CITY: Philadelphia
STATE: Pennsylvani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ALNAYYLPNKNQMVFPAGILQ-PTLYDPDFPQSLNYGGIGTIIGHELTHGYDGLGGPVPL
                                                                                                                                                                                                                        ZIP: 19103
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                         STREET:
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                       CLASSIFICATION:
                                           FILING DATE:
                                                                APPLICATION NUMBER: US/08/813,940
                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPACTGGTEASLQPXSCERLSASFPXLWTTFN-----VLQPGGERETXVWENIAVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08813940
                                                                                                                                                                                                                                                               Pennsylvania
                                                                                                                                                                                                                                                                                                      E: Woodcock Washburn Kurtz Mackiewicz & No.
One Liberty Place, 46th Floor
                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubin,
                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvey
                                                                                                                                                                                                                                                                                                                                                                         Composition, Reagents and Kits for Performing the Same : 25
                                                                                                                                                                                                                                                                                                                                                                                                                  Methods of Identifying Compounds that Inhibit DNA Synthesis in Mycobacterium Tuberculosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
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                                                                                                                                                                               513 LYHALRASNRIAIERGTHFKGFERS--KYASGEFFDKY----TDQIWEPKTQKVRQLFAD
                                                                                                                                                                                                                                                                        458
                                                                                                                                                                                                                                                                                                                                                                399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 VVVRVPQYFKDLFRI----LGSERKKTIANYL-----VWRMVYSRIPNLSRRFQYRWLEF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 VLESNIGPEGVWSERKFSLLQTLATFRGQ-----YSNSVFIRLYVSPDDKASNEHILKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 HNQDEKLDYLIRENYYER---EVLDQ----YSRNFVKTLLDRAYAK-----KFRFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 Match 2.9%; Score 116; DB 2; Length 725; Local Similarity 19.5%; Pred. No. 0.029; nes 139; Conservative 113; Mismatches 242; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                        FLSYAHVRCNSYRPEAAREQV----QIG-AHSPPQFRVNGAISNSEEFQKAF 731
                                                                                                                                                                                                                                                                     HQTHIKSVPSIEQGNNDS-----HAIGLGQMNLHGYLARERIFYGSDEGIDFTNIYFYTV 512
                                                                                                                                                                                                                                                                                                                                                              CSEILQVSTPSLFNEDLSYAKVGK-DISCNLGSLNIAKTMDSPDFAQTIEVAIRALTAVR 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVVIPDITFELAKRNDDMYLFS---PYDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDM 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESI-----GRSINSALQLSKRGGGV-----ALLTNIREHGGAIKNIENQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEIMIPHENRTSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPH---LKDISPSEN 338
                                                                                                                                 YYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLF 684
                                                                                                                                                                                                                        SYGAIGV---IVGHEFTH--GFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSN 624
                                                                                                                                                                                                                                                                                                                   -----KAVPKTEWFTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTE------YPRSL 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEKYYEMVDDARIRKTKIKAREFFQTLAELQFESGYPYIMFEDTVNRANPIDGKITHSNL 398
                                                                                        ----AGIRIPTQ-----DDWRRLKESVQAH-----
-ISYINHSTSSIHPIVSKVEVRKEGKIGRVYYPAPYMTN----DNLEYYEDAY 650
                                                                                                                                                                                                                                                                                                                                                                                                            -----VNEDLKAIKFSEADYFGNV--LQTRKYLAQSDF-----FWLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ERVYGVPFADISV 338
                                                                                             GIYNQNLQAVPPTGS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0652.0980002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 07/876,791
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
NUMBER OF SEQUENCES: 42
CORRESPONDENCES: 42
412 SALPYVVGKMFVDVYFQEDKKEMMEELVEGV-RWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                               257 K---NSLYGTLINISNEITKYSKMP--LGKGEYKYLDI-----VNLMSQLFYSKNYLQ 304
                                                                                                          360 KTIANYLVWRMV-----YSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
                                                                                                                                                                                              301 -NISELSAMIPOFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERK 359
                                                                                                                                                                                                                                         156 NYIYNNRLYLDNNSSITENKRNDVLSVKYNSILVFI-HENSKKNITYEELVQLISSKYSI 214
                                                                                                                                                                                                                                                                                                                               104 GEFSENNNIKI----KDSSFHKKDVKIDGQWLYKLVH--YLE--SDYTYYKDSFVIWNQQ 155
                                                                                                                                                                                                                                                                                                                                                                        196 GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL----Y 250
                                                                                                                                                         215 ENKEEVKVFVQEL----INKEIIFSDLRPTLENKNP----
                                                                                                                                                                                                                                                                                    251 KFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM----- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/392,625 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
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Kaletta, Cortina
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Schnell, No. 5837485bert
Augustin, Johannes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Augustin, Johann
Engelke, Germar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entian, Karl-Dieter
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	TELECOMMONICATION INFORMATION:	
	REFERENCE/DOCKET NUMBER: 0552.0980004  TELECOMMINICATION INFORMATION:	
	d, Robert W.	
	DATE: 31-0CT-1991	
	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/784.234	٠. ٠.
	ING DATE: 30-APR-1992	٠
	à	
	FILING DATE: 22-FEB-1995	
	7302	
	SSIFICATION: 435	
	6-JUN-	
	73 66	
	ARE: PatentIn Release #	٠.
	; COMPUTER: IBM PC compatible	
	TYPE: Floppy dis	
	; COMPUTER READABLE FORM:	
	TRY:	
	TATE:	
	STREET: 1100 New York Avenue, NW	
	Sterne, Kessler, Go	
	DENC	
	OF INVENTION: Chemical Compounds	
	OF INVENTION: Biosynth	
	; APPLICANT: Jung, G nther ; APPLICANT: Kellner, Roland	
	: Kupke, Th	
	ICANT: Wieland	
	; APPLICANT: Katerra, Corra	
	senstei	
	: Engelke, G	
	: Augustin, Johannes	
	; APPLICANT: G tz, Friedrich	
	: Entian, Karl	
	AL INFORMATION:	
	; Sequence 20, Application US/U8466961A ; Patent No. 5843709	
	961A-20	
	Db 547 YLYSEKH 553	
	Qy 684 FFLSYAH 690 :	
546	Db 505 LNSRNVNILNNNRIYNTCLNLNLPKSDIDINDIFIGATFNKL	
683	Qy 632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQL	
504	GRPTGNFNIKKKNQLQKEI	
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456	Db 398 IQNNSHIEITENDVKNLEKNNTVSKINAPVSTEIYSEIYFGNSIKGYEDFAVISPILGS-	
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9 1	Db 346NYHEFFM-DXYGFFOIVNIKOII SOINGEG VORFDGYVETSANTAFF FORVETS	
524	Qy 471 AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAOSDFFWLRKA	
345	Db 305IDTYIDYSRNELKQSLADNISEAAYILWLLSPHEFGTKTIR	

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RESULT 14
US-08-645-193B-15
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino according to the control of the control of
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
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                                                                                                                                                                                                                                                                                        APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEP-----LLPGITFTNNQL 683
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                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
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                                     COUNTRY: U.S.A.
                                                                                                                                                                                                      ADDRESSEE:
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20005
                                                                          D.C.
                                                                                                                                        E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
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19.6%; Pred. No. 0.07;
%ative 92; Mismatches 199; Indels 149;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 1
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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547 YLYSEKH 553
                                      684 FFLSYAH 690
                                                                                      505 LNSRNVNILNNN----
                                                                                                                        632 LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEP------LLPGITFTNNQL 683
                                                                                                                                                                                                                                                                                                 525 VPKTEW--FTNPTTVNAFYSASTNQIRFPAG-ELQKPFFWGTEYPRSLSYGAIGVIVGHE 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 KFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAMYNKM----- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 GQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDAL----Y 250
                                                                                                                                                                                                               582 FTHGFDNNGRKYDK-NGNLDPWWSTESEEKFKEKTKCMINQYSNY-----YWKKAG 631
                                                                                                                                                                                                                                                        398 IQNNSHIEITENDVKNLEKNNTVSKINAPVSTEIYSEIYFGNSIKGYEDFAVISPILGS- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                 305 -----IDTYIDYSRNELKQSLADNISEAAYILWLLSPNHF---GTKTIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 GEFSENNNIKI----KDSSFHKKDVKIDGQWLYKLVH--YLE--SDYTYYKDSFVIWNQQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                    ----FNAGATFGRFTGNF-----NIKKKNQLQKEIVHHYNNYMNENDLEISQLNEAP 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALPYVVGKMFVDVYFQEDKKEMMEELVEGV-RWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K---NSLVGTLINISNEITKYSKMP--LGKGEYKYLDI-----VNLMSQLFVSKNYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERK 359
                                                                                                                                                                                                                                                                                                                                            -----NYHEFFM-DKYGFEQLVNLKQLLSDINGFG-YPKKDSYSFSNNIAFLKEKYLLA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTIANYLVWRMV-----YSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENKEEVKVFVQEL----INKEIIFSDLRPTLENKNP------LDYIINSLNP 256
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19.6%; Pred. No. 0.07;
19.6%; Pred. No. 0.07;
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                                                                               -RIYNTCLN-----LNLPKSDIDINDIFIGATF--NKL
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30;

524 345 304

US-08-655-345-4 RESULT 15

Sequence 4, Application US/08655345

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	MVYSRIPNLSRREQYRWLEESRVIQGTTTLLPQWDKCVNFIESALPYVV 418	Qy 370 MVYSRIPNLS
	KRRADPDPMKNTCKLLVVADHRFYRYMGRGEESTTTNYLI	178
	LYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWR 369	Qy 326 LYPHLKDISP
	FVNDTKDKRMLVYKSEDIKNVSRLQSPKVCGYLKVDNEEL 177	
	NKMNISELSAM-IPQFDWL	Qy 270 DMKSVLRLEI
	VDGKNESEYTVKWQDFFTGHVVGEPDSRVLAHIRDDDVIIRINTDGAEY 130	Db 82 VDGKNESEYT
	KLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGAN	Qy 210 PDDKASNEHI
	LQTSTHVETLLTESALKVV 81	Db 43 LQTSTHVETL
	LRHSPFRWPVLESNIGPEGVWS	
	SFGPHQRLEKLDSLLSDYDILSLSNIQQHSVRKRD 42	Db 1 PRPPDDPGFGPH-
	PIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKAD 152	Qy 93 PIPEDMPSYG
38;	2.7%; Score 108; DB 2; Length 681; 18.9%; Pred. No. 0.16; vative 96; Mismatches 237; Indels 266; Gaps 38	Query Match Best Local Similarity Matches 140; Conser
	3: protein	; MOLECULE TYPE: US-08-655-345-4
	inear	7: 11
		; SEQUENCE CHARAC ; LENGTH: 681
	R SEQ ID 06: 4:	~~~
	O1	트딩
		REFERENCE/DOCKET
	N NTWHER 32.655	, NAME: Malaska, Step
	T INFORMATION:	; FILING DATE: 8-JUN-1995; ATTORNEY/AGENT INFORMATION:
	VITON DATA: V NUMBER: 08/428,458	י ע
	1995	FILING DATE:
	ATION DATA: AUTMBER: 08/504.614	; PRIOR APPLICATION DATA:
	E: TION: 435	; FILING DATE: ; CLASSIFICATIO
	NUMBER: US/08/655,345	; APPLICATION NUMBER: US
	rd for Apple, Version 6	SOFTWARE: M1
	COMPUTER: Apple Apple Operating System 7 5 2	COMPUTER: Ap
	ABLE FORM:	; COMPUTER READABLE
	· SA	; COUNTRY: USA ; ZIP: 98101
		; STATE: WA
	University Street	STREET: 51 University
	ADDRESS	CORRESPONDENCE A
	TNF-a CON	- 24
	March: Comidian B	
	Black, Roy A.	ICANT:
	42 TION:	; Patent No. 5830742 ; GENERAL INFORMATION:

	: 34 secs	rime	Job	
	Search completed: May 21, 2003, 18:50:38	rch co	Sea	
	PPPGNAEDDTVCLDLGKCK 557	539	Ф	
	PPNSTMNRGMDSCR 747	734	Qy	
538	NATCKGVSYCTGNSSEC	486	Дb	
733	NSYRPEAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNC	694	Qy	
485	436 CSKQSIYKTIESKAQECFQERSNKVCGNSRVDEGEECDPGIMYLNNDTCC 485	436	DЬ	
693	KRTLGENIADNGGLREAFR-AYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRC 693	637	Qy	
435	GAEHDPDGLAECAPNEDQGGKYVMYPIAVSGDHENNKMFSN 435	395	Db	
636	DNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKG 636	587	Qy	
394	AYYSPYGKKNIYLNSGLTSTKNYGKTILTKEADLVTTHELGHNF 394	351	망	
586	NPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGF	533	Qy	
350	AHLFTYQDFDMGTLGLAYVGSPRANSHGGV	318	В	
532	AKV-GYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFT 532	474	Qy	
317	YPNEEKDAWDVKMLLEQFSFDIAEEASKVCL 317	287	Ър	
473	GKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVL 473	419	Qy	

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
     Match Length DB
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     Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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US-09-978-295A-526
US-09-978-192A-526
US-09-978-192A-526
US-09-999-832A-526
US-09-978-189-526
US-10-174-590-420
US-10-175-737-420
US-10-175-738-420
US-10-175-738-420
US-10-176-757-420
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1238.005 Million cell updates/sec
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GENERAL INFORMATION:
APPLICANT: Fan Dennis Harrow
APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh

of sexual dysfunction

TITLE OF INVENTION: Compounds for the treatment FILE REFERENCE: PCS10926APME CURRENT APPLICATION NUMBER: US/09/905,846 CURRENT FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: 0017387.2 PRIOR FILING DATE: 2000-07-14 PRIOR PLICATION NUMBER: 60/220,908 PRIOR FILING DATE: 2000-07-26 NUMBER: 60/220,908 PRIOR FILING DATE: 2000-07-26 NUMBER: 05:8

SOFTWARE: FastSEQ for Windows Version 4.0

US-09-905-846-2

Sequence 2, Application US/09905846 Patent No. US20020102707A1

<b>4</b> . U	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223	1223
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-10-176-487-42	-10-176-485-42	-10-176-481-42	-10-175-747-42	4	-10-174-585-	US-10-174-576-420	-10-173-705-	-10-173-697-	-10-173-695-	-10-184-658-	-176-993-	-10-176-992-	-176	-10-176-987-42	-10-176-985-42	-10-176-750-4	-176-747-4	-10-176-492-4	-10-176-48	-175-743-4	-175-740-4	-175-739-4	4-588-4	-174-582-4	79-4
Sequence 420,		420,		420,	420,	420,	420,	420,	420,		420,	420,	420,		420,	420,	420,		•	Sequence 420,	`	420,	420,	e 420,	420,
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## ALIGNMENTS

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; SEQ ID NO 2
LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-846-2
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219 ILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLL--GANSSR----AEHDMK 272
                                            194 EVYGGWPVAMDR-----WNETYGLEWELERQLALMNSQFNRRYLIDLFIWNDDQNSSRH 247
                                                                                                                                   137
                                                                                                                                                         102 GYYPWLRHNVDLKLKELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILR 161
                                                                                                                                                                                                                 HSPFRWPVLESNIGPEGVWSER----KFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEH 218
                                                                                                                                 SIFDVLRDELEVILKAVLENSTA--KDRPAVEKARTLYRSCMNQSVIEKRGSQPLLDIL- 193
                                                                                                                                                                                                                                                                                                                          33.7%; Score 1332.5; 39.2%; Pred. No. 3.86
                                                                                                                                                                                                                                                                                                                            2.5; DB 10; Length 779; 3.8e-100;
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US-09-978-295A-526
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                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         627 WKKAG-LNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFF 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QALNEGGIGMVIGHEITHGFDDNGRNEDKNGNMADWWSNESTQHEREQSECMIYQYGNYS
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Hillan, Kenneth J
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                REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH
                                                                 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILLING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064311
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DR FILLING DATE: 1998-03-20
DR APPLICATION NUMBER: 60,078936
DR FILLING DATE: 1998-03-20
DR APPLICATION NUMBER: 60,078910
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Baker Kevin P.
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Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Desnoyers, Luc
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R APPLICATION NUMBER: 60/08
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DR FILING DATE: 1998-04-21 OR APPLICATION NUMBER: 60/080105
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OR APPLICATION NUMBER: 60/080165
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OR APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838 APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081195 APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/084640
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FILING DATE: 1998-05-06
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    KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
                                                                            EAETGSSV--ETGKKANRGTRIAL-VVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCL 55
                                        ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66
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267; Conserv
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                                                                                                 REAFRAYRKWINDRROGLEEPLLPGITFTNNOLFFLSYAHVRCNSYRPEAAREQVQIGAH 710
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SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736
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                        SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                            KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH
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RESULT 4
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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                                               Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                             Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                         Ferrara, Napoleon Filvaroff, Ellen
                                                                                                                  Gerritsen, Mary E.
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                                                                                                                                                                                                                Desnoyers, Luc
Pan, James;
                      Kuo, Sophia S.
                                   Kljavin,
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           Napier,
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DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080165
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DR APPLICATION NUMBER: 60/080194
DR FILING DATE: 1998-03-31
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PAPPLICATION NUMBER: 60/079689

OR FILING DATE: 1998-03-27

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OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR PETLING DATE: 1998-03-11
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OR APPLICATION NUMBER: 60/077641
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Wood, William
NUMBER: 60/080333
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RR APPLICATION NUMBER: 60/08
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RR FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554 APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: FILING DATE: 1998-0. APPLICATION NUMBER: APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/083496 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 APPLICATION NUMBER: APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: FILING DATE: 1998-04-23 APPLICATION NUMBER: APPLICATION NUMBER: 6 FILING DATE: 1998-04-APPLICATION NUMBER: FILING DATE: 1998-04-APPLICATION NUMBER: FILING DATE: 1998-04 APPLICATION NUMBER: FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/ FILING DATE: 1998-04 APPLICATION NUMBER: 1998-04-27 NUMBER: 60/084639 1998-05-07 1998-04-29 1998-04-29 1998-04-29 1998-04-28 1998-04-1998-04-09 1998-04-08 1998-04-08 .998-04-09 60/084637 60/084441 60/084414 60/084366 60/083499 60/082796 60/082797 60/083392 60/082700 60/082804 60/082704 60/082569 60/081955 60/081229 60/081203 60/081195 60/081071

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Best Local :
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531 FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG 590
                                                                                                                      406 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464
                                                                                                                                                                                                                                                                                                                          292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GWNITGPWDQDNF--MEYLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR
                                                                                                                                                                                                                                                                                                                                                                                                            233 EDYLDNSTEAKSYRDALYKFMYDTAYLLGANSSRAEHDMKSYLRLEIKIAEIMIPH-ENR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER:
FILING DATE: 1998-0:
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                                                                               AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085704
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FILING DATE: 1998-05-15
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FILING DATE: 1998-05-07
                                           AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524
                                                                                                                                                             ESALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKAR 470
                                                                                                                                                                                                      ELINRTEPSILNNYLIWNLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNT 405
                                                                                                                                                                                                                                            RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
                                                                                                                                                                                                                                                                                     DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP-----LELSDSEPVVVYGMDYLQQVS 345
                                                                                                                                                                                                                                                                                                                                                                     DYYL-NRTANEKYLTAYLDYMEELGMLLGGRPTSTREQMQQYLELEIQLANITVPQDQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P---EGVWSERKFSLLQTLATERGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHLLENT-TFNSSSEAEQKTQRFYLSCLQYERIEELGAQPLRDLI-----EKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085579
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FILING DATE: 1998-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.9%; Score 1223; DB 9; 35.2%; Pred. No. 3e-91; tive 145; Mismatches 307;
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RESULT 5
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APPLICANT: Ashkenaz
                                                     PRIOR PRIOR PRIOR
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                                                                                                                                         PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/062250
PRIOR TILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILING DATE: 2001-10-24 PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 SMTPQTVNAYYLPTKNEIVFPAGILQAPFY-ARNHPKALNFGGIGVVMGHELTHAFDDQG
APPLICATION NUMBER: 60,077649
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60,077791
FILING DATE: 1998-03-12
                                                                                                     APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
                                                                 FILING DATE: 1998-03-1
                                                                                    APPLICATION NUMBER:
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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o. US20020192706A1
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01 PRIOR PRIOR PRIOR PRIOR PRIOR RIOR DR APPLICATION NUMBER: 60/079939
DR FILING DATE: 1998-03-25
DR APPLICATION NUMBER: 60/079294
DR APPLICATION NUMBER: 60/079656
DR FILING DATE: 1998-03-26
DR APPLICATION NUMBER: 60/079664
DR APPLICATION NUMBER: 60/079669
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079669
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079663
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079728
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OR FILING DATE: 1998-03-31 OR APPLICATION NUMBER: 60/080333
OR FILING DATE: 1998-04-01
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OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/081070
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081049
OR FILING DATE: 1998-04-08 DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/082568
DR FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/C
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APPLICATION NUMBER: 60/C APPLICATION NUMBER: 60/078004 FILLING DATE: 1998-03-13 APPLICATION NUMBER: 60/078886 FILLING DATE: 1998-03-20 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-20 APPLICATION NUMBER: 60 FILING DATE: 1998-04-1 APPLICATION NUMBER: 60 APPLICATION NUMBER: 60/080327 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078936 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-15 FILING DATE: 1998-04
APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-04-15 FILING DATE: 1998-04-09 APPLICATION NUMBER: APPLICATION NUMBER: NUMBER: 1998-04-09 1998-04-15 60/078910 60/080194 60/081203 60/081838 60/081952 60/081819 60/081817 60/081195 60/081229 60/081071 60/081955

PRIOR DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083554
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083558
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DR APPLICATION NUMBER: 60/084639
DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084640
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DR APPLICATION NUMBER: 60/084598
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DR APPLICATION NUMBER: 60/085580
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DR APPLICATION NUMBER: 60/085573
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DR APPLICATION NUMBER: 60/085704
DR APPLICATION NUMBER: 60/085704
DR FILING DATE: 1998-05-15 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22 FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-27 APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER: FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/082700 APPLICATION NUMBER: APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-22 APPLICATION NUMBER: FILING DATE: 1998-0 FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: FILING DATE: 1998-04-29 APPLICATION NUMBER: FILING DATE: 1998-04-29 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/085338 1998-04-1998-04-29 1998-05-06 1998-05-13 1998-05-1 998-04-60/083495 60/083336 60/083545 60/083392 60/082797 60/085579 60/085689 60/085323 60/084637 60/084441 60/083499 60/083496 60/083322

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                                                                                                                                                                                                                         Sequence 526, Application US/09978189 Publication No. US20030004102A1
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                                                                                                                                                                                                                                                                                                                                          699 SPARFRYLGTLSNSRDFLRHFGCPYGSPMNPG-QLCEVW 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYYL-NRTANEKYLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL
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                       Fong, bill-
Gao, Wei-Qiang
                                                                                                                                Botstein, David
Desnovere
                                                                       Filvaroff, Ellen
Gerritsen, Mary E
                     Gerber, Hanspeter
                                                                                                                Eaton, Dan
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR TILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 50/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR ETILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR ETLING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077791
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/078939
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     APPLICATION FILING DATE:
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Hillan, Kenneth J
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                         NUMBER:
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1998-03-27
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   NUMBER: 60/080107
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PRIOR APPLICATION NUMBER: 1998-04-15
PRIOR FILING DATE: 1998-04-15
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DR APPLICATION NUMBER: 60/082796

DR FILING DATE: 1998-04-23

DR APPLICATION NUMBER: 60/083336

DR FILING DATE: 1998-04-27
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083499
FILING DATE APPLICATION
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082700
FILING DATE: 1998-04-22
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081229
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FILING DATE: 1998-04-15
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FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/085339
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; ORGANISM: Homo Sapien
US-10-174-590-420
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Best Local Similarity
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LENGTH: 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
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175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232
                                      176 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
                                                                                                                         116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG
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                                                                                    KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI------EKIG 174
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Goddard, Audrey
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; ORGANISM: Homo Sapien US-10-176-758-420
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                                                                                                                                                 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 420
LENGTH: 736
TYPE: PRT
     Matches 267; Conservative 145; Mismatches 307;
                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME EILE REFERENCE: 93430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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                      30.9%; Score 1223; DB 9; Length 736; 35.2%; Pred. No. 3e-91;
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul :
APPLICANT: Gurney, Austin 1
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                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50 CURRENT APPLICATION NUMBER: US/10/175,737 CURRENT FILING DATE: 2002-06-19
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Application removed - See File Wrapper or
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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US-10-173-706-420

Sequence 420, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
APPLICANT: Baker, Keyin P.

APPLICANT:

Chen, Jian Desnoyers, Luc Goddard, Audrey

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                                                                                                                                                                                                                                                      FTNPTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNG
                                    SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                        KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH
                                                                                                              REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH
                                                                                                                                                    REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL
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SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736
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LENGTH: 736
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CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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                                                                               REAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAH
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                                      KAAYNAYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPH
                                                                                                                                                                         RKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGL
SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                              REYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQY--QVNGERLNGRQTLGENITDNGGL
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LENGTH: 736
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Best Local
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CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW
                                   AVLAKVGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEW
                                                                                                                                                                                    RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFI 410
                                                                                                                                                                                                                                                                                                 DYYL-NRTANEKYLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR
                                                                          DDALGFALGSLFVKATFDRQSKETAEGMISETRTAFEEAL-GQLVWMDEKTRQAAKEKAD
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Godowski, Paul
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Pred. No. 3e
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US-10-175-752-420
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CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
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  292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP---
                                        292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
                                                                                                                                                                        175 GWNITGPWDQDNF--MEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR 232
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                                                                                 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR
                                                                                                                        EDYLDNSTEAKSYRDALYKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
                                                                                                                                                                                                                 P---EGVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVR 232
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LENGTH: 736
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CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                        Prior Application removed - NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
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                                                                                                    56 KPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKL 115
                                                                                                                                                                                                                                                      Local Similarity
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                 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG
                                                          TEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL 126
                                                                                                                                              ELGAGSNYGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHSTCL 66
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Godowski, Paul
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                                                                                                                                                                                                                                                  30.9%; Score 1223; DB 9; 35.2%; Pred. No. 3e-91;
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US-10-176-757-420
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US-10-176-757-420
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                                                                       SEQ ID NO 420
LENGTH: 736
TYPE: PRT
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 420, Application US/10176757 Publication No. US20030022297A1
                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C86
                                                                                                                            Prior Application removed NUMBER OF SEQ ID NOS: 612
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
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Gurney, Austin L.
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Godowski, Paul
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                                                                                                                                                                                                                                                                                                         Smith, Victoria
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   INVENTION: SECRETED
                                                                                                                                    Desnoyers, Luc
Goddard, Audrey
                     Zhang, Zemin
                                     Wood, William I.
                                                   Smith, Victoria Watanabe, Colin K.
                                                                                      Pan, James
                                                                                                    Godowski, Paul
Gurney, Austin
                                                                                                                                                                     Chen, Jian
                                                                                                      F. J
   AND
TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; P1Or Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612 .
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-420
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                                                                                                                                                                                                      584
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                                                                                                                                                                                                                                                                                                                                                                                                                                       233 DYYL-NRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 GWNITGPWDQDNF--MEYLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 KHLLENT-TFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLI------EKIG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 DEEKIYHKMSISELQALAPSMDWLEFLSFLLSP-----LELSDSEPVVVYGMDYLQQVS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 TSEAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 KELLEKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIG 175
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                                                               SPARFRVLGTLSNSRDFLRHFGCPVGSPMNPG-QLCEVW 736
                               SPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                   ELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQXHRDPSHSTCL 66
                                                                                                                                                                                                                                                                                                                                                 DDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAFEEAL-GQLVWMDEKTRQAAKEKAD 464
                                                                                                                                                                                                                                                                            AIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQW 524
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Search completed: May 21, Job time : 64 secs

2003, 18:55:13

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:45:44; Search time 48 Seconds (without alignments)
1500.098 Million cell updates/sec

Title: US-09-913-955A-1
Perfect score: 3958
Sequence: 1 MEAETGSSVETGKKANRGTR......AFNCPPNSTMNRGMDSCRLW 749

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	<b>_</b>	No.	Result
442	494	495	502	511.5	512.5	547.5	567	599.5	606	646.5	899	672	778	814.5	949	997	1014.5	1119.5	1184	1241.5	1243.5	1248.5	1257	1257	1260	1263.5	1283.5	1351	Score	
11.2	12.5	12.5	12.7	12.9	12.9	13.8	14.3	15.1	15.3	16.3	16.9	17.0	19.7	20.6	24.0	25.2	25.6	28.3	29.9	31.4	31.4	31.5	31.8	31.8	31.8	31.9	32.4	34.1		Ouerv
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protein T06D4.5 [i hypothetical prote		hypothetical prote		hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable zinc meta	hypothetical prote	hypothetical prote	endopeptidase O [i	endopeptidase O (E	protein F18A12.6 [

## ALIGNMENTS

356 SERKKITANYLYWRMYYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALP 	NKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG :: : :	Qy 245 YRDALYKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY 29	Qy 185 FSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 24 	Qy 128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPERWPVLESNIGPEGVWSERK 18 	Qy 68 SKVNLSVDPCDNFFFFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR 1:	Qy 18 GTRIALVVFVGGTL-VLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAIL 6: 	Query Match 34.1%; Score 1351; DB 2; Length 774; Best Local Similarity 38.2%; Pred. No. 1.4e-83; Matches 289; Conservative 156; Mismatches 266; Indels 46; Gaps	A;Contents: Brain and testis A;Accession: UC7265 A;Molecule type: mRNA A;Residues: 1-774 <tan> C;Genetics: A;Gene: nepII C;Superfamily: neprilysin C;Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropept:</tan>	(EC 3.4.24.11) II - rat Rattus norvegicus (Norway rat) Aug-2000 #sequence_revision 18-Aug-2000 #text_change (     JC7265 ; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; pphys. Res. Commun. 271, 565-570, 2000 prilysin II: A putative novel metalloprotease and its number: JC7265
NFIESALP 415 :::   : SYVNSNME 443	KDLFRILG 355 ::   : ENLEEIID 383	RTS-EAMY 297    :    H:1	DNSTEAKS 244 :: KEDSHR 267	WSERK 184  :	EKSISRRR 127     :   EDSSVQHR 158	IEAAAAIL 67 :        VIAAARIL 98	74; 46; Gaps 18;	neuropeptide; testis;	e 02-Sep-2000 C.; Schwartz, J.C. ts isoforms in CNS and
	356 SERKKTIANYLVWRMYYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESALP	298 NKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILG :: : : : : : : : : : : : : : : : : : :	245 YRDALYKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTS-EAMY	185 FSILQTLATERGQYSNSVFIRLYVSPDDKASNEHILKLDOATLSLAVREDYLDNSTEAKS	128 DTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERK	68 SKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRR ::               :::           :::             :::	18 GTRIALVVFVGGTL-VLGTILFLVSOGILSLQAKOEYCLKPECIEAAAAII	Query Match  Best Local Similarity 38.2%; Pred: No. 146-83;  Matches 289; Conservative 156; Mismatches 269; Indels 46; Gaps  18 GTRIALVVFVGTTL-VCGTILFLYSGLLSLQAKQEYCLKPECIEAAAAII 67	CONCENTES: BEALM AND CESTIS ACCESSION: JO7265 AC

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A; Molecule type: mRNA
A; Residues: 2-191;211-737 < LET>
A; Cross-references: EMBL: Y00811
A; Note: part of this sequence, including the amino end of the mature protein,
A; Note: part of this sequence, including the amino end of the mature protein,
A; Note: part of this sequence, including the amino end of the mature protein,
A; Malfroy, B; Kuang, W.J.; Seeburg, P.H.; Mason, A.J.; Schoffeld, P.R.
PEBS Lett. 229, 206-210, 1988
PEBS Lett. 229, 206-210, 1988
A; Title: Molecular cloning and amino acid sequence of human enkephalinase (neu A; Reference number: S00350; MUID: 88152222; PMID: 3162217
A; Accession: S00350
                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Y00811; NID:g29625; PIDN:CAA68752.1; PID:g29626 R;Letarte, M.; Vera, S.; Tran, R.; Addis, J.B.L.; Onizuka, R.J.; Quackenl J. Exp. Med. 168, 1247-1253, 1988
A;Title: Common acute lymphocytic leukemia antigen is identical to neutra A;Reference number: JL0084; MUID:89010526; PMID:2971756
A;Accession: JL0084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neprilysin (EC 3.4.24.11) [validated] - human
N;Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase (Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A41387; A36173; S05275; JL0084; S00350; S02228
R;D'Adamio, L.; Shipp, M.A.; Masteller, E.L.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 7103-7107, 1989
A;Title: Organization of the gene encoding common acute lymphoblastic leukemia ant. A;Reference number: A41387; MUID:89386688; PMID:2528730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M26605
A;Note: the authors translated the codon AAC for residues 14 and 72 as Asp
R;Shipp, M.A.; Richardson, N.E.; Sayre, P.H.; Brown, N.R.; Masteller, E.L.; Clayton, L.R
Proc. Natl. Acad. Sci. U.S.A. 85, 4819-4823, 1988
A;Title: Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA) id
A;Reference number: A36173; MUID:88263038; PMID:2968607
A;Accession: A36173
       A; Molecule type: n
A: Residues: 3-750
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-750 < JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A; Reference number: S05275 A; Accession: S05275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-750 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Jongeneel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: part of this sequence was confirmed by protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:J03779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-750 <DAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKYRVLGSLQNLPGFSEAFHCPRGSPMH-PMNRCRIW 774
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C;Keywords: glycoprotein; hydrolase; metalloproteinase; F;2-750/Product: neprilysin *status experimental <MAT>F;16-23/Region: stop-transfer sequence
F;29-51/Domain: transmembrane *status predicted <TMN>F;29-51/Domain: extracellular *status predicted <EXT>F;145,285,311,325,335,628/Binding site: carbohydrate (Asf;884,588/Binding site: zinc (His) *status predicted F;585/Active site: Glu *status predicted
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A;Note: 467-Thr was also found
C;Comment: This enzyme inactiva
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A; Introns: 54/1; 66/1; 120/1; 147/1; 179/1; 218/3; 240/3;
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A;Cross-references: GDB:120190; OMIM:120520
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                                                                                                                                                                                                                                                                                                        534 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
                                                                                                                                                                                                                                                                                                                                                                                                                                        475 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 PYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 NISELSAMI-----POFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 EKATAQINSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSR-DYYECTGIYKEACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSER----KFSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 KKKORWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIONM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV
                                                                                                                                                                                                                                                    AAVVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRNF
AYRAYONYI--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP
                                                          AFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP
                                                                                                                            NKDGDLVDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQ
                                                                                                                                                                                      DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE
                                                                                                                                                                                                                                                                                                                                                                             RIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG
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R;Malfroy, B.; Schofield, P.R.; Kuang, W.J.; Seeburg, P.H.; Mason, A.J.; Blochem. Blophys. Res. Commun. 144, 59-66, 1987
A;Title: Molecular cloning and amino acid sequence of rat enkephalinase. A;Reference number: A29295; MUID:87213218; PMID:3555489
A;Accession: A29295
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F:16-23/Region: stop-transfer sequence
F:29-51/Domain: transmembrane *status predicted <TMN>
F:52-750/Domain: extracellular *status predicted <EXT>
F:145,285,325,628/Binding site: carbohydrate (Asn) (covalent) *status predicted F:311/Binding site: carbohydrate (Asn) (covalent) *status experimental F:584,588/Binding site: zinc (His) *status predicted F:585/Active site: Glu *status predicted F:585/Active site: Glu *status predicted
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A;NOte: part of this sequence, including the amino end of the mature protein, was R;Bateman Jr., R.C.; Jackson, D.; Slaughter, C.A.; Unnithan, S.; Chai, Y.G.; Moom J. Biol. Chem. 264, 6151-6157, 1989
A;Title: Identification of the active-site arginine in rat neutral endopeptidase
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C;Date: 30-Sep-1992 #sequence_revision 3
C;Accession: A29295; A33521
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A; Residues: 95-102, 'X', 104-129 <BAT>
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A; Residues: 1-750 <MAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: neprilysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: This enzyme inactivates a variety of peptide hormones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
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Matches
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                                                             360 TKYSPRDLQNLMSWRFIMDLVSSLSRNYKESRNAFRKALYGTTSETATWRRCANYVNGNM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 DASAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
                                                                                                                     GSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIESAL
                                                                                                                                                                                TLAKLQNNFSLEINGKPFSWSNFTNEIMSTVNI----NIQNEEEVVVYAPEYLTKLKPIL
                                                                                                                                                                                                                                        NISELSAMI-----PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVQKAKTLYRSCINESAIDSRGGQPLLTLL-PDIYGWPVASQN------WEQTYGTSWTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSE---RKFSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKQRWTPLEISLSV---LVL--LLTIIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
                                                                                                                                                                                                                                                                                                   AYVDFMISVARLIRQEQRLPIDENQLSLEMNKVMELEKEIANATTKPEDRNDPMLLYNKM
                                                                                                                                                                                                                                                                                                                                                       ALYKEMVDTAVL-----LGANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSE-AMYNKM 300
                                                                                                                                                                                                                                                                                                                                                                                                                     EKSIAQLNSKYGKKYLINFFVGTDDKNSTQHIIHFDQPRLGLPSR-DYYECTGIYKEACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1263.5; DB
Pred. No. 1.2e-77
1; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-Sep-1992 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface antigen
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Moomaw, C.
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715 GNFRIIGTLQNSAEFADAFHCRKNSYMNPER-KCRVW 750
                      713 PQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                  658 AYRAYQNYV--KKNG-EEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSP
                                                                                                                          653 AFRAYRKWINDRROGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSP 712
                                                                                                                                                                    598 NKDGDLVDWWTQQSANNFKDQSQCMVYQYGNFTWDLAGGQHLNGINTLGENIADNGGIGQ
                                                                                                                                                                                                              594
                                                                                                                                                                                                                                                    AAVVNAFYSSGRNQIVFPAGILQPPFF-SARQSNSLNYGGIGMVIGHEITHGFDDNGRNF
                                                                                                                                                                                                                                                                                 PTTVNAFYSASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKY 593
                                                                                                                                                                                                                                                                                                                                         RIGYPDDIISNENKLNNEYLELNYKEEEYFENIIQNLKFSQSKQLKKLREKVDKDEWISG 538
                                                                                                                                                                                                                                                                                                                                                                                                                             ENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLD-DLTWMDAETKKKAEEKALAIKE 478
                                                                                                                                                                                                          DKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKA-GLNVKGKRTLGENIADNGGLRE
                                                                                                                                                                                                                                                                                                                                                                                 KVGYP-EFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                               652
                                                                                         714
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A; Note: part of this sequence, including the amino end of the mature protein, R; Kahn, P.H.; Powell, J.F.; Beaumont, A.; Roques, B.P.; Mallet, J.J. Biochem. Biophys. Res. Commun. 145, 488-493, 1987.
A; Title: An antibody purified with a lambda GT11 fusion protein precipitates (A; Reference number: 146872; MUID:87241544; PMID:3297057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalin A;Reference number: A29451; MUID:87275825; PMID:2440677
A;Accession: A29451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neprilysin (EC 3.4.24.11) - rabbit
N;Alternate names: CD10; common actute lymphocytic leukemia antigen; endopeptidase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A29451; I46872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 207-275 <KAH>
A; Cross-references: GB:M16593; NID:9165556; PIDN:AAA53694.1; PID:9165557
C; Comment: This enzyme inactivates a variety of peptide hormones, cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Devault, A.; Lazure, C.; Nault, C.; Le Moual, H.; EMBO J. 6, 1317-1322, 1987
                                                                                                                                                                                                                                                                                                                                                                                                   F;52-751/Domain: extracellular #status predicted CEXT>
F;145,286,312,326/Binding site: carbohydrate (Asn) (covalent)
F;585,589/Binding site: zinc (His) #status predicted
F;586/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-751 <DEV>
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                                                                                                                                                                                                                                                                                                                                                                            F;629/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;16-23/Region: stop-transfer sequence F;29-51/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;2-751/Product: neprilysin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X05338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: neprilysin
   74
                                                           71
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                                                                                                                                                                                                                                                                                Local
                                                           NLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTE 130
                                                                                                                                                                                 KKANRGTRIALVVFVGGTLVLGTILFLVSQGLLSLQAKQE--YCLKPECIEAAAAILSKV 70
DATAEPCTDFFKYACGGWLKRNVIPETSSRYSNFDILRDELEVILKDVLQE--PKTEDIV 131
                                                                                                                         KKKQRWTPLEISLSV---LVL--LLTVIAVTMIALYATYDDGICKSSDCIKSAARLIQNM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antig
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                  Conservative 149;
                                                                                                                                                                                                                                                                                31.8%;
36.0%;
                                                                                                                                                                                                                                                                      Score 1260; DB 1;
Pred. No. 2e-77;
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                             Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #status
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A;Gene: GDB:ECE1; ECE
A;Cross-references: GDB:698357; OI
A;Map position: 1p36.1-1p36.1
C;Superfamily: neprilysin
C;Keywords: alternative splicing;
F;57-77/Domain: transmembrane #stt.
F;154.175,198,258,304,350,371,527;
F;595,599/Binding site: zinc, catt
F;596/Active site: Glu #status pre
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                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-758 <SHI>
A;Cross-references: GB:D43698; NID:g1197803; PIDN:BAA07800.1; PID:g1197804
A;Experimental source: umbilical vein endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                        endothelin converting enzyme c;Species: Homo sapiens (man) C;Date: 17-May-1995 #sequence C;Accession: JC2551 R;Shimada, K.; Matsushita, Y.
                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 207, 807-812, 1995
A;Title: Cloning and functional expression of human endothelin-converting A;Reference number: JC2521; MUID:95169128; PMID:7864876
A;Accession: JC2521
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;Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; ;57-77/Domain: transmembrane #status predicted <TMM>;57-77/Domain: transmembrane #status predicted <TMM>;154,175,198,258,304,350,371,527,620,639/Binding site: carbohydrate (Asn) (cc;595,599/Binding site: zinc, catalytic (His) #status predicted;596/Active site: Glu #status predicted
                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGNFRIIGSLANSVEFSEAFQCPKNSYMN-PEKKCRVW 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAYRAYQNYV--KKNG-EEKLLPGIDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAFRAYRKWINDRRQGLEEPLLPGITFINNQLFFLSYAHVRCNSYRPEAAREQVQIGAHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAIVNAFYSSGRNQIVFPAGILQPPFF-SAQQSNSLNYGGIGMVIGHEITHGFDDNGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                      K.; Matsushita, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 3.4.24.-) 1, umbilical vein endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                 Wakabayashi, K.; Takahashi, M.; Matsubara, A.; 207, 807-812, 1995
                                                                                                                                                                         OMIM: 600423
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NSKEFSEHFRCPPGSPMN-PPHKCEVW
                             NSEEFQKAFNCPPNSTMNRGMDSCRLW
                                                                                           DRRQGLEEPLLPGITFTUNQLFFLSYAHVRCUSYRPEAAREQVQIGAHSPPQFRVNGAIS
                                                                                                                            WKNSSVEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
                                                                                                                                            WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN
                                                                                                                                                                                                                          ASTNQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW
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                                                            -KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS
                                                                                                                                                                                            PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW
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RESULT 6

endotnelin converting (man)
C;Species: Homo sapiens (man)
C;Date: 31-Aug-1995 #sequence\_revision 27-Oct-1995 #text\_change 20-Jun-2000
C;Accession: JC4136; S51009; S47269
R;YOrimitsu, K; Moroi, K; Inagaki, N.; Saito, T.; Masuda, Y.; Masaki, T.;
Biochem. Biophys. Res. Commun. 208, 721-727, 1995
A;Title: Cloning and sequencing of a human endothelin converting enzyme in A.Paference number: JC4136; MUID:95209687; PMID:7695628 A; Molecule type: mRNA A; Rosidues: 1-770 < YOR> A; Cross-references: GB:D49471; NID:g695404; PIDN:BAA08442.1; PID:g695405 A; Experimental source: renal adenocarcinoma cell A; Experimental source: renal adenocarcinoma cell A; Note: it is uncertain whether Met-1 or Met-18 is the initiator R; Schmidt, M.; Kroeger, B.; Jacob, E.; Seulberger, H.; Subkowski, T.; Oti endothelin converting enzyme (EC 3.4.24.-) 1, renal adenocarcinoma Y.; Masaki, T.; Seino, T.; Otter, R.; Meye

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Query Match

31.8%;

Score 1257;

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Length

723

NSEEFQKAFNCPPNSTMNRGMDSCRLW 749

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A;Cross-references: GDB:698357; OMIM:600423
A;Map position: 1p36.1-1p36.1
C;Superfamily: neprilysin
C;Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase;
F;69-89/Domain: transmembrane #status predicted <TMM>
F;69-89/Domain: transmembrane (Thr) (covalent) #status predicted
F;165,187,210,270,316,362,383,339,632,651/Binding site: carbohydrate (Asn) (co
F;607,611/Binding site: zinc, catalytic (His) #status predicted
F;608/Active site: Glu #status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Molecular characterization of human and bovine endothelin converting A;Reference number: S51009; MUID:95104423; PMID:7805846 A;Accession: S51009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 18-770 <SC2>
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                                                                                                               WSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWIN 662
                                                                                                                                                                                                         ASTNQIREPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPW
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                                        DRRQGLEEPLLPGITFTUNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQFRVNGAIS 722
                                                                                       WKNSSYEAFKRQTECMVEQYSNY--SVNGEPVNGRHTLGENIADNGGLKAAYRAYQNWV-
                                                                                                                                                                               PTKNEIVFPAGILQAPFYTRSS-PKALNFGGIGVVVGHELTHAFDDQGREYDKDGNLRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSKSIATE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGDEEAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSYACGGWIKANPVPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKAQVYYR
-KKNGAEHS-LPTLGLTNNQLFFLGFAQVWCSVRTPESSHEGLITDPHSPSRFRVIGSLS
                                                                                                                                                                                                                                                                                                                                                              IILEIKKAFEESL-STLKWMDEETRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTA
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Pred. No. 3.4e-77;
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C;Superfamily: neprilysin
C;Keywords: hydrolase; metalloproteinase; transmembrane protein;
F;57-77/Domain: transmembrane *status predicted <TMM>
F;595,99/Binding site: zinc, catalytic (His) *status predicted
F;596/Active site: Glu *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:U27342; NID:g897601; PIDN:AAA82928.1; PID:g897602 R;Ikura, T.; Sawamura, T.; Shiraki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, E Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994 A;Title: cDNA cloning and expression of bovine endothelin converting enzyme. A;Reference number: JC2448; MUID:95032010; PMID:7945289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C;Accession: A54667; JC2448
R;Xu, D.; Emoto, N.; Giaid, A.; Slaughter, C.; Kaw, S.; deWit, D.; Yanagisan
Cell 78, 473-485, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-90,'A',92-698,'A',700-758 <IKU>
A;Cross-references: GB:S73774; NID:g688289; PIDN:AAB32062.1; PID:g688290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A54667; A; Accession: A54667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: ECE-1: a membrane-gound metalloprotease that catalyzes the proteolytic A; Reference number: A54667; MUID:94340737; PMID:8062389
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                            FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRDTEAIQKAKILYSSC 142
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                                              DLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSAS
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                                                                                       LEIKKAFEESL-STLKWMDEDTRKSAKEKADAIYNMIGYPNFIMDPKELDKVFNDYTAVP
                                                                                                                                EGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIM-----
                                                                                                                                                                                                                      RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV
                                                                                                                                                                                                                                                                 -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ
                                                                                                                                                                                                                                                                                                                                                    GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF---
                                                                                                                                                                                                                                                                                                                                                                                NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK
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                                                                                                                                                                            RFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENTLGFALGPMFVKATFAEDSKNIASEII
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FNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPT
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J. Biol. Chem. 269, 18275-18278, 1994

A;Title: Cloning and functional expression of endothelin-converting enzyme from rat endo A;Reference number: A53679; MUID:94308046; PMID:8034569

A;Accession: A53679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endothelin converting enzyme (EC 3.4.24.-) - rat C;Speciles: Rattus norvegicus (Norway rat) C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000 C;Accession: A53679; JU0189 R;Shimada, K.; Takahashi, M.; Tanzawa, K.
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F;150,171,194,254,300,346,367,523,616,635/Binding site: carbohydrate (Asn) (covalent)
F;591,595/Binding site: zinc, catalytic (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;592/Active site: Glu #status predicted
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A; Residues: 1-754 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 LVVLV-TLLAAGLVACLAALGIQYRTRTPPVCLTEACVSVTSSILNSMDPTVDPCQDFFS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
RFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALPYVVGKMFVDVYFQEDKKEMMEELV
                                                                                                                                                                                                                                                                                                           FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMYDTAVLL-G
                                                                                                                                                                           GDEDSIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPFLNA
                                                                                                                                                                                                     ANSSRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK
                                                                                                                                                                                                                                                                                                                                                                              MNETRIEELRAKPLMELIEKLG-GWNI-----TGPWAKDNFQ--DTLQVVTAHYRTSP
                                                                                                                                                                                                                                                                                                                                                                                                           MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV
                                                                           I----FYP--VEINESEPIVVYDKEYLRQVSTLINSTDKCLLNNYMMWNLVRKTSSFLDQ
                                                                                                                                                                                                                                                                            FFSVYVSADSKNSNSNVIQVDQSGLGLPSRDYYL-NKTENEKVLTGYLNYMVQLGKLLGG
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A;Cross-references: EMBL:235306; NID:g535074; PIDN:CAA84547.1; PID:g535075 C;Superfamily: neprilysin C;Keywords: hydrolase; metalloproteinase; zinc F;591,395/Binding site: zinc, catalytic (His) #status predicted F;592/Active site: Glu #status predicted
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A; Residues: 1-754 <SC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Schmidt, M.; Kroeger, B.; Jacob, E.; Seulberger, H.; Subkowski, T.; Otter, R.; Meye FEBS Lett. 356, 238-243, 1994
A;Title: Molecular characterization of human and bovine endothelin converting enzyme A;Reference number: S51009; MUID:95104423; PMID:7805846
A;Accession: S51010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine C;Species: Bos primigenius taurus (cattle) C;Decies: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999 C;Accession: S51010; S47268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 LVVLV-ALLAAALVACLAVLGIQYQTRTPSVCLSEACISVTSSILSSMDPTVDPCQDFFT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKPECIEAAAAILSKVNLSVDPCDNFFR 82
                                                                                                                                                                                                                                                                                                                MNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLATFRGQYSNSV 202
                                                                                                                                                                                                                                                                                                                                                               YACGGWIKANPYPDGHSRWGTFSNLWEHNQAIIKHLLENSTA--SVSEAERKDQEYYRAC
                                                                          GAEDTIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF---
                                                                                                                     NS-SRAEHDMKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISELSAMIPQFDWLGYIKK 320
                                                                                                                                                                                                                 FIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVLLGA 262
                                                                                                                                                                                                                                                                   MNETRIEELKAKPLMELIEKLG-GWNI-----TGPWDKDNFQ--DTLQVVTSHYHTSP
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endothelin converting enzyme (EC 3.4.24.-) 2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Sep-1999
C;Accession: I46078
R;Emoto, N.; Yanagisawa, M.
J. Biol. Chem. 270, 15262-15268, 1995
A;Title: Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-sensitive in A;Reference number: A57042; MUID:95318093; PMID:7797512
A;Accession: I46078
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C;Superfamily: neprilysin
C;Keywords: hydrolase; metalloproteinase
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A;MoLecule type: mRNA
A;Residues: 1-825 <EMO>
A;Cross-references: EMBL:U27341; NID:g897599; PID:g897600
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLKAIKFSEADYFGNVLQTRKYLAQSDFFW-----LRKAVPKTEWFTNPTTVNAFYSAS 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REQUADEKEMEVMYGTKKTCLPRWKECVSDTENTLGFALGPMEVKATFAEDSKNIASEII 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LNTIFYP--VEINESEPIVIYDKEYLSKVSTLINSTDKCLLNNYMIWNLVRKTSSFLDQ 392
                                                                                                                                                                                                                                                                                             EAGFRKRTSRLLGLHTQLELVL-AGVSLLLAALLLGCLVALGVQYHRDPSHSTCLTEACI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                      NT-TFNSSSEAERKTQRFYLSCLQVERIEELGA----HALRD-----LIDKIGGWNVT 268
                                                                                                                                                                           KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPERWPYLESNIG---PE 177
                                                                                                                                                                                                                                                                                                                              ETGSSVETGKKANRGTRIALVVFVGGTLVLGTILF--LVSQGL-LSLQAKQEYCLKPECI 60
                                                                                                                                                                                                                                                        EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                       GPWDQDNE -- MEVLKAVAGTYRATPFFTVYVSADSKSSNSNIIQVDQSGLFLPSRDYYL-
                                                                                             GVWSERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLD 237
                  NSTEAKSYRDALYKFMVDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPH-ENRTSEAM
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                       29.9%; Score 1184; DB 2; llarity 35.1%; pred. No. 3.4e-72; Conservative 138; Mismatches 313;
313;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 825;
                                                                                                                                                                                                                                                                                                                                                                                Indels 38;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Molecule type: DNA
A;Residues: 1-750 <STO>
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C; Superfamily: neprilysin
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C;Genetics:
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                      117 LLDENDEPYDYETSAVGKAKYFYNLCLNESEILDNWRTTFDEVVK-SFGGWPSLGHOMKP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656
                                                           118 LL-EKSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           드
                                                                                                                                      58 ECIEAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKE 117
                                                                                                     GCIKTASVILSSMNSSVDPCDDFYEFACGQWIKGHPIPDDAPSVSNFENIGQDLEFALKE 116
                                                                                                                                                                                                                                                                250;
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297 YNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 FALGSLFVKATFDRQSKEIAEGMISEIRVAFEEAL-GHLVWMDEKTRQAAKEKADAIYDM 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 NRTANEKVLTAYLDYMEELGMLLGGQPTSTREQMRQVLELEIQLANITVPQDQRRDEEKI 385
                                                                                                                                                                                                                                                                                                                                                                                              596 NGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGYPEFIMNDTHVNEDLKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHKMSIAELQALAPSMDWLEFLSFLLSP-----LELGDSEPVVVYGTDYLQQVSELINR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVNAYYLPTKNEIVFPAGILQAPFY-TCNHPQALNFGGIGVVMGHELTHAFDDQGREYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVNAFYSASTNOIREPAGELOKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEPSVLNNYLIWNLVQKTTSSLDHRFESAQEKLLETLYGTKKSCTPRWQTCISNTDDALG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGT-TTLLPQWDKCVNFIESALP 415
RYLGTLSNSRDFLRHFGCPYGSPMNSG-QLCEVW 825
                                                                           RVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                           AYKAWL--RKHG-EEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGLVTDPHSPARF
                                                                                                                                                                                                                              AYRKWINDRRQGLEEPLLPGITFTUNQLFFLSYAHVRCNSYRPEAAREQVQIGAHSPPQF 715
                                                                                                                                                                                                                                                                                                                   EGNLRPWWQNESLAAFRNHTACIEEQYSQY--QVNGEKLNGRQTLGENIADNGGLKAAYN 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGFPDFILEPKELDDVYDGYEVSEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677
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protein T05A8.4 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001 C;Accession: D88082 R;anonymous, The C; elegans Sequencing Consortium. A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/Projects/C\_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 Match 28.3%; Score 1119.5; D Local Similarity 32.4%; Pred. No. 7e-68; 4 DEEDGTTKSPG----SRWTRIWAIIALILLILFLLVLGAAIYF----YINYKDSSDVCLSP 56 2 EAETGSSVETGKKANRGTR----IALVVFVGGTLVLGTILFLVSQGLLSLQAKQEYCLKP 57 Conservative 150; Mismatches GB:chr\_II; PIDN:AB95021.1; PID:g2746865; GSPDB:GN00020; CESP:T05A 324; DB 2; Indels Length 750; 47; Gaps 15;

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A:Map position: 2
A:Introns: 11/1; 334/3; 439/1; 692/2; 734/2
C:Superfamily: neprilysin
                                                                                                                                                                              A;Cross-references: EMBL:269904; PIDN:CAA93782.1; GSPDB:GN00020; CESP:ZK20.6
A;Experimental source: clone ZK20
                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-766 <WI2>
                                                                                                                                          A; Gene: CESP: ZK20.6
                                                                                                                                                                                                                                                                       A/Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, March 1996
A;Reference number: 219209
A;Accession: 720003
A;Status: preliminary; translated from GB/EMBL,
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK20.6 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T20003; T27775
R;Gajadsty, S.
                                                                                                                                                                                                                                                                                                      A; Reference number: 220417
A; Accession: T27775
                                                                                                                                                                                                                                                                                                                                                                      A:Experimental source: clone C47D12 R;Gajadsty, S.
                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-766 <WIL>
A;Cross-references: EMBL:Z69902; PIDN:CAA93770.1; GSPDB:GN00020; CESP:ZK20.6
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T20003
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                                                                                                                                                                     Genetics:
                               Query Match
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701 KEAIRKLRTSEHSPGPIRVKGPLSNSYDFAKAYNCEPGSQMN-PREKCRVW 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644 TKGENIADNGGLKQAYRAYKKY---EKRHSRPPRLPGVNLTHDQLFFLNYAQIWCGTMND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     699 EAAREQVQIGAHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 TLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPGITFTNNQLFFLSYAHVRCNSYRP 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 GHEITHGFDDRGRLYDNLGNIRQWWDNATISKFEHKAQCIEKQYSSYVLDQINMQINGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 KRKIGYPDYLNDPAAVNNEYKTFKVYPGHYYQTKFSFYEQYQRDVLERITEAVDRERWVA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 LYTKITLGEMRRSLPHFNWPLFFNRMFKDLHEKNGKRITFDDNTEVVVYGYEFLRRLDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKR 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAALVNAFYSPNTNEISKFLGTLTQKFKFSVFPAGILQ-PVFYSKDFPSSMNFGGIGVVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPYVVGKMFVDVYFQEDKKEMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAV
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    25.6%;
Score 1014.5; DB Pred. No. 9.6e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---FPAGELQKPFFWGTEYPRSLSYGAIGVIV 578
                     2
                   Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-Jan-2000
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A; Molecule type: DNA
A; Residues: 1-590 <STO>
                                                                                                                                                                                                                   A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                              protein F18A12.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                   A; Map position:
                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                      R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                     A;Cross-references:
                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                              A; Accession: C88099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C88099
                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 MLKQIGYPDFILNDEKLDDWYKGLEGAPEDSFSQLVE-KSIQWRNNFYYRRLLEPVNRFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 DNTS-IPTSKSIALIKQIYNTCMDTEKHNAVGARDLLEKIKTYGY-WPMVHNE----KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHSPPQFRVNGAISNSEEFQKAFNCPPNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRQFDNVGNLRDWWDNTTSSKFNERTQCIIEQYADVKLRGTDLRINGKLTQGENIADNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRKYDKNGNLDPWWSTESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKQAFKAYKSYL--EKHGGQEARLPQFESLTNEQLFFVGYAQVWCGAKTPETKTLLLLTD 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LREAFRAYRKWINDRRQGLEEPLLPGI-TFTNNQLFFLSYAHVRCNSYRPEAAREQVQIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKLSYASGSMYVRKYFDANAKNTTLDMITDLQEAFRNMMH-ANDWMDAETKKYALEKADQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RILGSERKKTIANYLVWRMVYSRIPNLSRRFQYRWLEFSRVIQGTTTLLPQWDKCVNFIE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYTKLYNVRRFDDLKEYMSIIDWKKLTLSTTPFLVHSYLK-TNPS--IIISDVEYLQKMN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-EAMYNKMNISELSAMIPQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLF 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKYEKQMKAYRKYTIGKVRYYTEDAG-MAVNESKIESDVDEIIAFEKEWAQILVAEEDRR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---STEAKSYRD---ALYKFMYDTAVLLGANSSRAEHDMKSVLRLEIKIAEIMIPHENRT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSL--AVREDYLDN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESTFDLTKLLSNTIQSRDVSVFFDFGPAEDSRNVSRRLLSFDQGSLGLGYSTRDYYLDE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSISRRRDTEAIQKAKILYSSCMNEKAIEKADAKPLLHILRHSPFRWPVLESNIGPEGVW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EASRLLQKSLNLSLDPCDDFFEYACRAWVDSHPIPDDLTSYSQFTATREKVLAEMRKLYE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAAAAILSKVNLSVDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223;
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                                                                                                         GB:chr_II; PIDN:AB66079.1; PID:g2315629; GSPDB:GN00020;
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Score 997;
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Query Match

25.2%;

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Length

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RESULT 14

T24949

T24949

hypothetical protein T16A9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text,
C;Accession: T24949
R;McMurray, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19959
A;Accession: T24949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-769 <WIL>
A;Residues: 1-76
                                                                                                                                                                                                                              A;Cross-references: EMBL:277135; PIDN:CAB00879.1; GSPDB:GN00023; CESP:T16A9. A;Experimental source: Clone T18A9 C;Genetics: C;Genetics: A;Gene: CESP:T16A9.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
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                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMIMHLRNSFADLV-RQNDWMDEETKAVAIEKANSMINNIGYPDVTNDLPKLDKQYLGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPLFETLTELG-EWPLLQEN-----WDKTKFNFTSLLVNSRRDYGVDVFFQLYIYADSK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNSTMNRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEEPLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPPFFSGT-FPKAVNYGAIGAVIGHEITHGFDDQGSQYDKDGNLHNWWSESSLNSFDTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWSTESEEKFKEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISDSDTYYYIMKKSVVWMQSREFQKLTKPFDKHEFDISPAVVNAFYSPEKNAITFPAGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLDERFEDIKQDFLKVMTGQQQSPPRWKDCAQVPSTVLPLAAGAIYVQAHFQESDKHEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PFFQSIAPSDLTHLFHNETEIIICEIEYLQHVSELIEKTDVGLLTNYVLWRVVQSNVR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYPHLKDISPSE-----NVVVRVPQYFKDLFRILGSERKKTIANYLVWRMVYSRIP 376
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                                                             Similarity
                                                                                                                                               neprilysin
                                                                                                                                                                   59/1; 105/3; 202/1; 336/3; 371/3; 393/1; 424/2;
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                                24.0%; Score 949; DB 2; 30.6%; Pred. No. 2.7e-56; Live 147; Mismatches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120;
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                                      277;
                                                                                    Length 769;
                                Indels
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F87683
                                                                                                                                                                                           R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelber, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; In J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87683
A; Gene: CC3504
C; Superfamily:
                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-706 <STO>
                                                       A;Cross-references: GB:AE005673; NID:g13425232; PIDN:AAK25466.1; GSPDB:GN00148C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87683
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                                                                624
                                                                                                666
                                                                                                                                                                                                                                                                              486 THVNEDLKAIKFSEADYEGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSAST 545
                                                                                                                               569
                                                                                                                                                              909
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                                                                                                                                                                                                                                                                                                                                                                                          341 YTDNAAPLLSKRFVDAGFEFRNKTLAGQPEQRPKWKRGVGAVNGLLGEAVGKDYVAAYFP 400
                                                                                                                                                                                                                                                                                                                                                                                                                           370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 KAKILYSSCMNEKAIEKADAKPILHILRHSPFRWPVLESNIGPEGVWSERKFSLLQTLAT 193
682 GWYSAYDVKPGDKLYIAPENR----VKIW 706
                            726 EFOKAFNCPPNSTM-----NRGMDSCRLW 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 FRGQYSNSVF---IRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 KYGAAYRAFMDEAGIEKLDAKPI-----APYLAEI-----RKVKSKDEFTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 VKPGEDFYKFANGAWDARTQIPSDRTRYGNFDKLAELSEARTKAIIEAAAANKAATGDTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 VSQGLLSLQAKQEY-CLKPECI------EAAAAI-----LSKVNLS 73
                                                         PESKAKMLELVANVRGAMKVRIDNL----DWMSAETKVKAQEKLAKFTVKIGYPD----- 451
                                                                                                                                                  ESEEKFKEKTKCMINQYSNYYWKKAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRR 665
                                                                                                                                                                                                             NQIRFPAGELQKPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWWST 605
                                                                                                                                                                                                                                                         --VWEDYSKLEIKDNDAYGNVQRAGAWAFAKDVERLFKPVDKTEWGMTPQTVNAYYNSVN 509
                                                                                                                                                                                                                                                                                                                                                                                                               MVYSRIPNLSRRFQYRWLEF-SRVIQGTTTLLPQWDKCVNFIESALPYVVGKMFVDVYFQ 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGYDWNRYIA-----ASGLPKVDRFVVTTNTTFPKYAKIYAETPLDTLKAWQAFK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQFDWLGYIKKVIDTRLYPHLKDISPSENVVVRVPQYFKDLFRILGSERKKTIANYLVWR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDPCDNFFRFACDGWISNNPIPEDMPSYGVYPWLRHNVDLKLKELLEKSISRRRDTEAIQ 133
                                                                                                                                                                                            EDKKEMMEELVEGVRWAF---IDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPEFIMND 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMGKSSTTPFTSLLGLGISTDAKNPKAYAVYAGAGGLSLPDRDYYLDAKFADKK---AAY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLSAFGAQAHEKHACIDDACVMQSLLPSITAGGAAADVASLESPRFGTWGFDLSGMDTT 73
                                                                                                                             EDAAKFKAQADRIGAQYGAFE-PIPGMKINGALTMGENIGDMGGLAFALDAYRASI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 706;
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Search completed: May 21, 2003, 18:50:01 Job time : 52 secs